

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
stomach
thyroid
spinal cord
lymph node
trachea
adrenal gland
bone marrow
spleen
thymus
prostate
testis
ovary
small intestine
colon
peripheral blood leukocyte

Fig. 1. Northern analysis of hepsin mRNA in human tissues. Northern hybridization was performed with multiple human tissues blots (CLONTECH) using a full-length human hepsin cDNA. Hepsin mRNA was detected in samples from liver, kidney, pancreas, stomach, thyroid, prostate and testis.

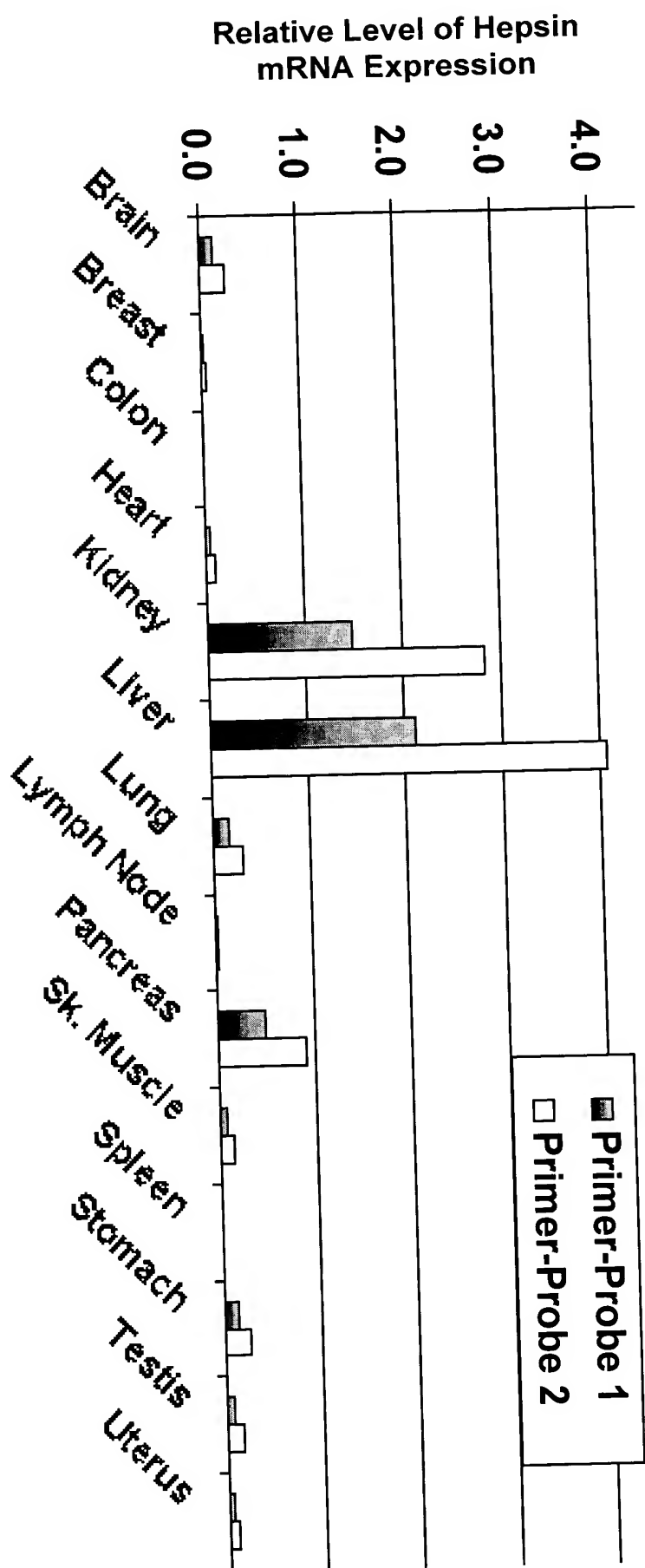
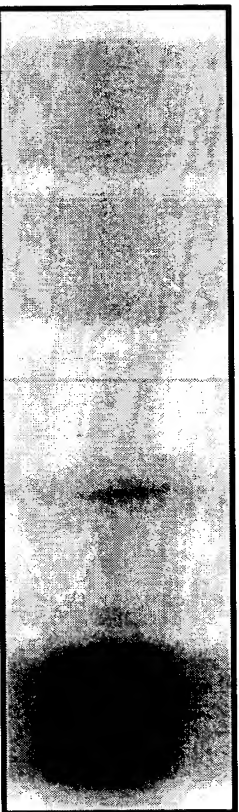


Fig. 2. Taqman analysis of hepsin mRNA expression in human tissues. Taqman-based quantitative PCR analysis of hepsin mRNA expression was performed using two sets of hepsin-specific primers (Primer-Probes 1 and 2). High levels of hepsin mRNA expression were detected in samples from liver and kidney.



Normal

Normal

BPH

**Primary
cancer**

**Advanced
cancer**

hepsin

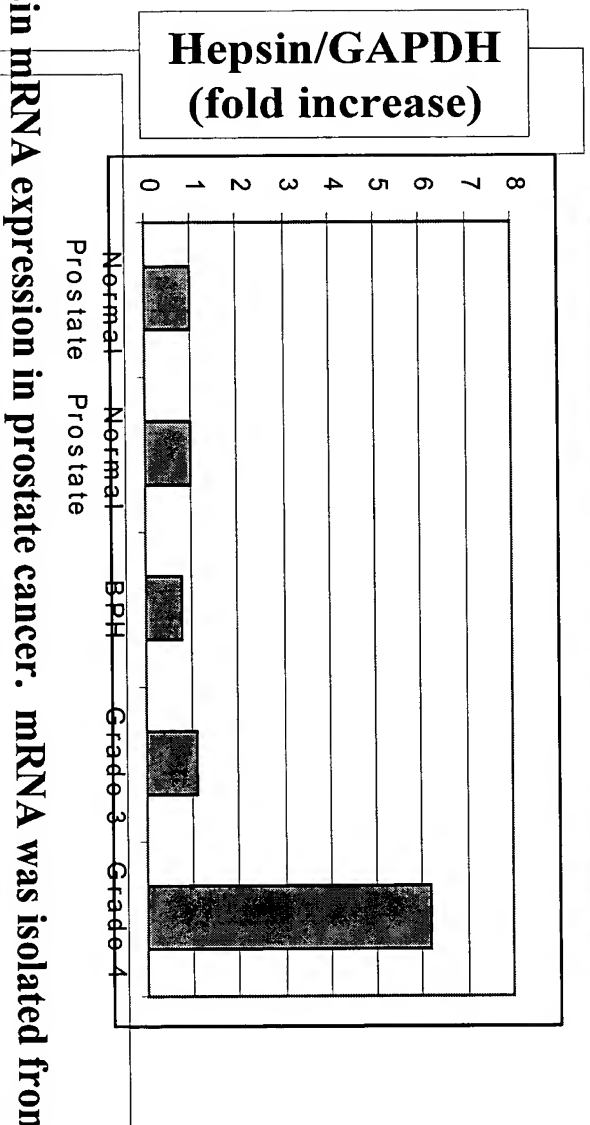


Fig. 3. Hepsin mRNA expression in prostate cancer. mRNA was isolated from normal prostate, BPH and prostate cancer tissues. Northern blot was prepared and hybridized with a human hepsin cDNA probe. Hepsin mRNA expressed was significantly higher in an advanced prostate cancer sample. The ratio of hepsin/GAPDH mRNA was ~6-fold higher in the advanced cancer than in normal prostate, BPH or primary prostate cancer.

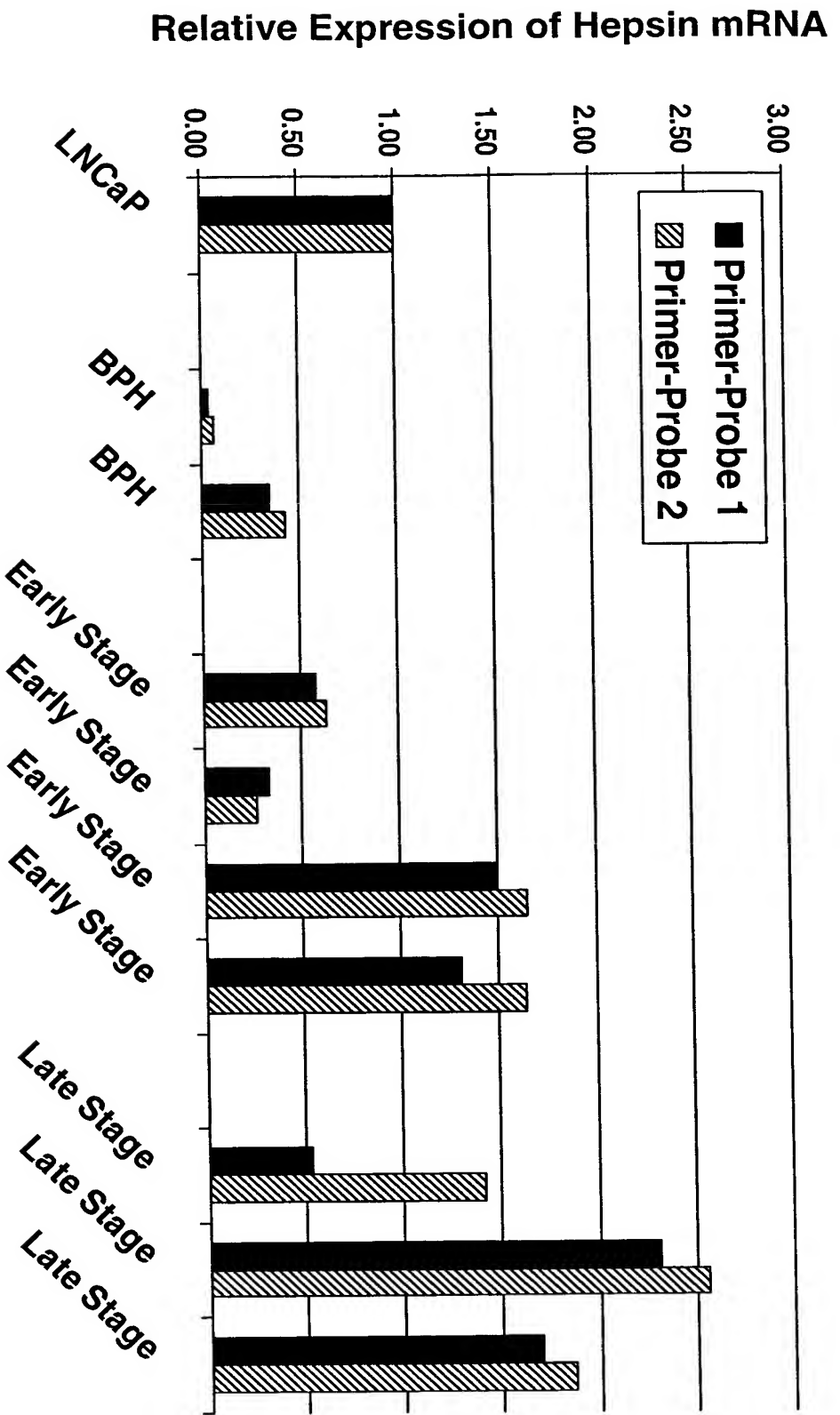


Figure 4. Taqman analysis of hepsin mRNA expression in prostate tissue. mRNA samples were prepared from LNCaP cells, BPH and prostate cancer (Gleason grade 3 and 4) tissues. Quantitative PCR analysis was performed using two set of primers specific for human hepsin (Primer-Probes 1 and 2). Modest to more dramatic increases of hepsin mRNA expression were detected in prostate cancer samples.

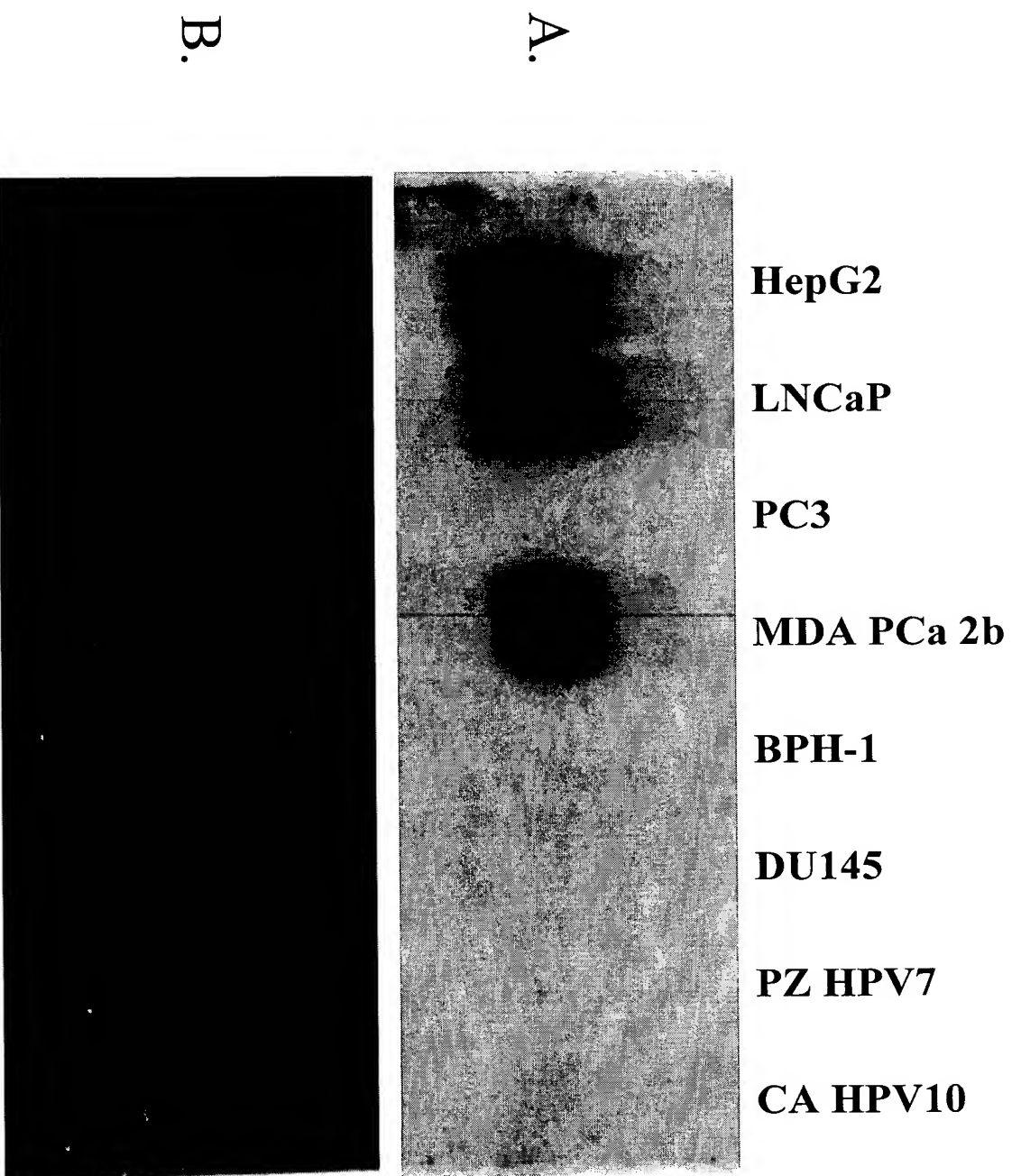


Fig. 5. Northern analysis of hepsin mRNA expression in prostate-derived cell lines. mRNA was isolated from prostate-derived cell lines, LNCaP, PC3, MDA PCa2b, BPH-1, DU145, PZ HPV7, CA HPV10 and a control cell line, HepG2. Northern analysis detected hepsin mRNA expression in LNCaP, MDA Pca 2b and HepG2 cells (upper panel). As a control, the agarose gel was stained with ethidium bromide to show equal sample loading.

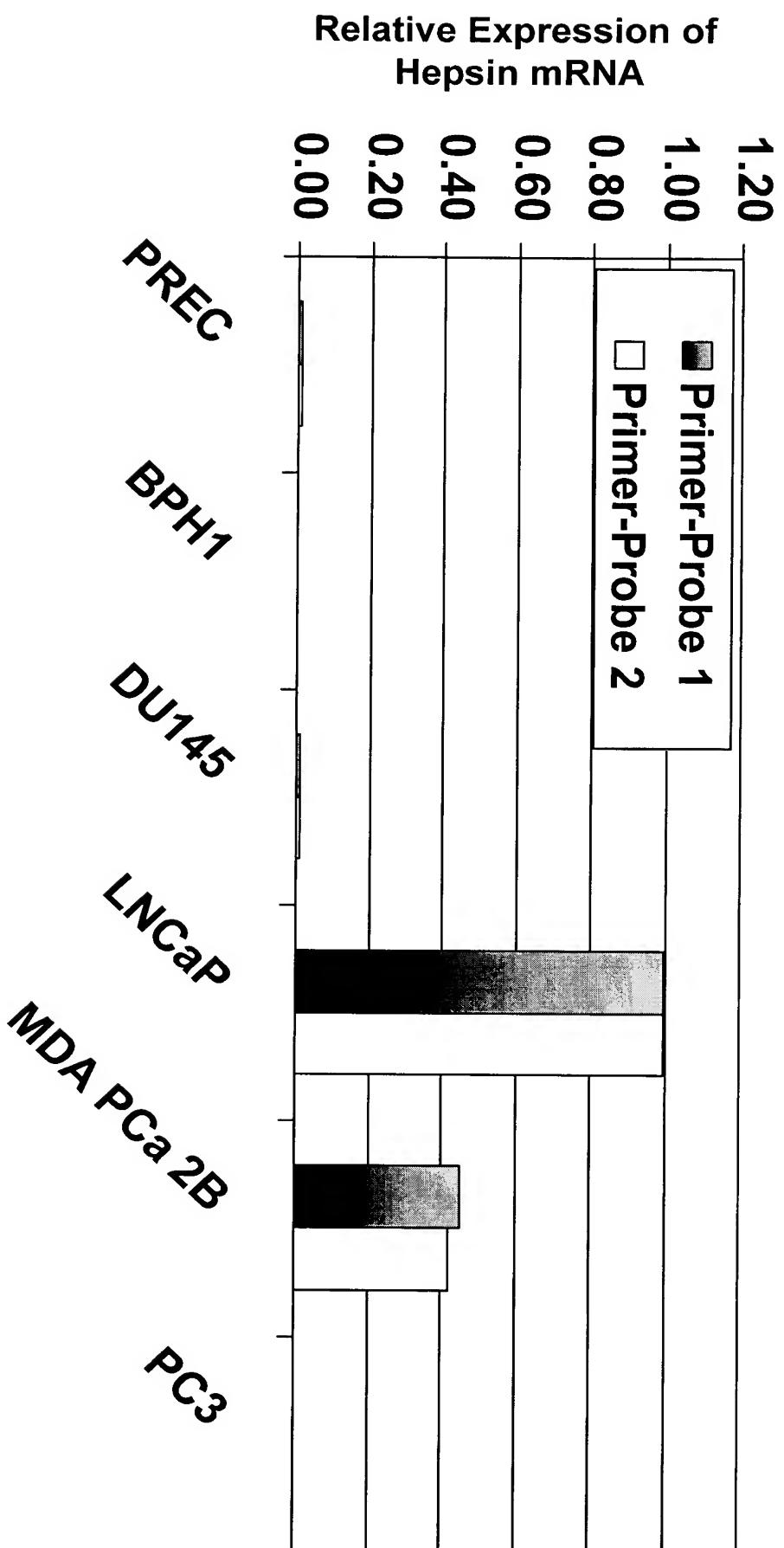
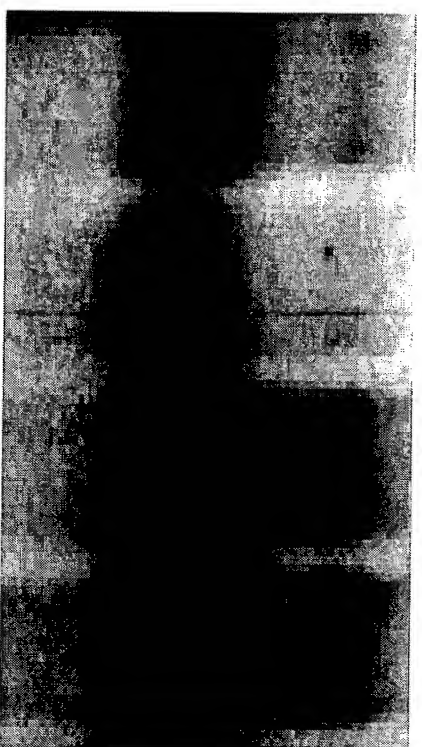


Fig. 6. Taqman analysis of hepsin mRNA expression in prostate-derived cell lines. mRNA was isolated from prostate-derived cell lines. Taqman analysis was performed using two sets of hepsin specific primers (Primer-Probes 1 and 2). Hepsin mRNA expression was detected in LNCaP and MDA Pca 2B cells.

A.



Hepsin

B.

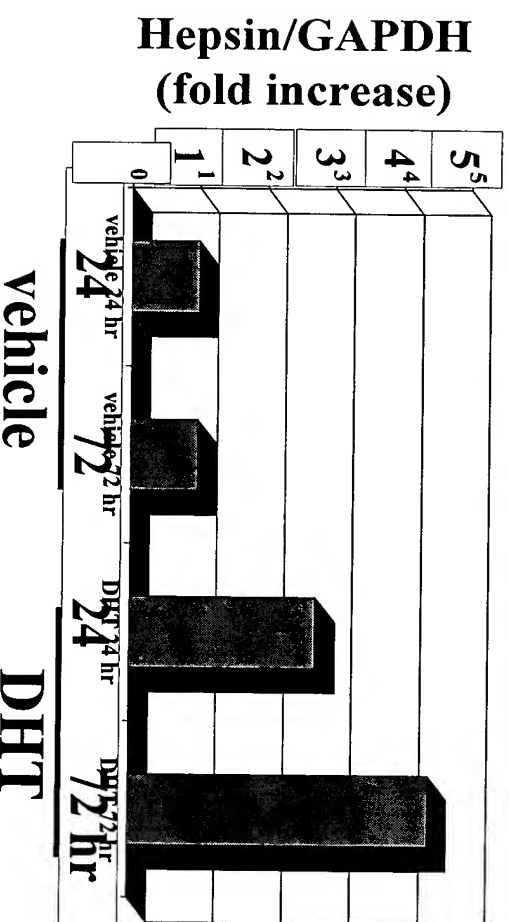


Fig. 7. Up-regulation of hepsin mRNA expression in LNCaP cells by dihydrotestosterone (DHT). LNCaP cells were treated with DHT (10 nM) and harvested at indicated time points. Total RNA samples were isolated. Northern blots were hybridized with a human hepsin cDNA probe and re-probed with a GAPDH cDNA. Hepsin mRNA expression was significantly enhanced in LNCaP cells treated with DHT for 24 and 72 hours.

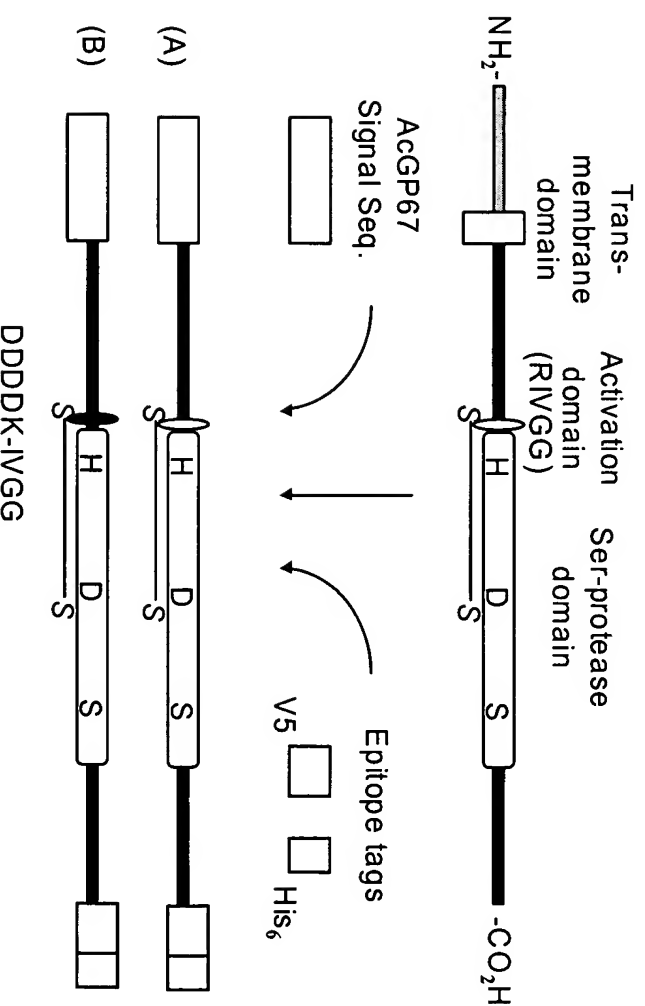


Fig. 8. Expression of soluble wild-type and mutant hepsins. A schematic presentation of human hepsin protein is shown on top. To express soluble wild-type hepsin (A), the extracellular domain of hepsin is cloned into vector pAcGP67 that contains a sequence coding for a signal peptide at the 5' end and a sequence coding for a V5 epitope and a His6 tag at the 3' end. In construct B, a sequence coding for an enterokinase recognition peptide, DDDDK, is inserted to replace the coding sequence for Arg 162. The mutation will allow hepsin to be activated by enterokinase.

FIG 9 (1-7) pIRESpuro2W/hepEK_k

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1  GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC
   CTGCCTAGCC CTCTAGAGGG CTAGGGGATA CCAGCTGAGA GTCATGTTAG
51  TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT
   ACGAGACTAC GGCCTATCAA TTCGGTCATA GACGAGGGAC GAACACACAA
101 GGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG
   CCTCCAGCGA CTCATCACGC GCTCGTTTTA AATTCGATGT TGTTCGGTTC
151 GCTTGACCGA CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG
   CGAACTGGCT GTTAACGTAC TTCTTAGACG AATCCCAATC CGCAAAACGC
201 CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT GATTATTGAC
   GACGAAGCGC TACATGCCCG GTCTATATGC GCAACTGTAA CTAATAACTG
251 TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA
   ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT
301 TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG
   ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG ACCGACTGGC
351 CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
   GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA
401 AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT
   TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTG ATAAATGCCA
451 AAAGTGGCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC
   TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG
501 CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA
   GGATAACTGC AGTTACTGCC ATTTACCGGG CGGACCGTAA TACGGGTCAT
551 CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA
   GTACTGGAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT
601 TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
   AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT
651 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
   ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT
701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
   ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT
751 ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
   TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC
801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
   CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC
851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTTGGTACC
   CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGAACCATGG
+3
901 GAGCTCGGAT CGATATCGCC ACCATGGAGA CAGACACACT CCTGCTATGG
   CTCGAGCCTA GCTATAGCGG TGGTACCTCT GTCTGTGTGA GGACGATACC
+3  V L L L W V P G S T G D A P D R S
951 GTACTGCTGC TCTGGGTTCC AGGTTCCACT GGTGACGCTC CGGACAGGAG
   CATGACGACG AGACCCAAGG TCCAAGGTGA CCACTGCGAG GCCTGTCTCT
+3  S D Q E P L Y P V Q V S S A D A R L
1001 TGACCAGGAG CCGCTGTACC CAGTGCAGGT CAGCTCTGCG GACGCTCGGC
   ACTGGTCCTC GGCACATGG GTACACGTCCA GTCGAGACGC CTGCGAGCCG

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FIGURE 9-1

pIRESpuro2W/hepEK_k

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+3  L M V F D K T E G T W R L L C S S
1051 TCATGGTCTT TGACAAGACG GAAGGGACGT GCGGCTGCT GTGCTCCTCG
    AGTACCAGAA ACTGTTCTGC CTTCCCTGCA CCGCCGACGA CACGAGGAGC
+3  R S N A R V A G L S C E E M G F L
1101 CGCTCTAACG CCAGGGTAGC CGGACTCAGC TGCGAGGAGA TGGGCTTCCT
    GCGAGATTGC GGTCCCATCG GCCTGAGTCG ACGCTCCTCT ACCCGAAGGA
+3  L R A L T H S E L D V R T A G A N G
1151 CAGGGCACTG ACCCACTCCG AGCTGGACGT GCGAACGGCG GGCGCCAATG
    GTCCCGTGAC TGGGTGAGGC TCGACCTGCA CGCTTGCCGC CCGCGGTTAC
+3  G T S G F F C V D E G R L P H T Q
1201 GCACGTCGGG CTTCTTCTGT GTGGACGAGG GGAGGCTGCC CCACACCCAG
    CGTGCAGCCC GAAGAAGACA CACCTGCTCC CTTCCGACGG GGTGTGGGTC
+3  R L L E V I S V C D C P R G R F L
1251 AGGCTGCTGG AGGTCATCTC CGTGTGTGAT TGCCCCAGAG GCCGTTTCTT
    TCCGACGACC TCCAGTAGAG GCACACACTA ACGGGGTCTC CGGCAAAGAA
+3  L A A I C Q D C G R R K L P V D D D
1301 GGCCGCCATC TGCCAAGACT GTGGCCGCAG GAAGCTGCCC GTGGACGACG
    CCGGCGGTAG ACGGTTCTGA CACCGGCGTC CTTGACGGG CACCTGCTGC
+3  D D K I V G G R D T S L G R W P W
1351 ACGACAAGAT CGTGGGAGGC CGGGACACCA GCTTGGGCGG GTGGCCGTGG
    TGCTGTTCTA GCACCCTCCG GCCCTGTGGT CGAACCCGGC CACCGGCACC
+3  Q V S L R Y D G A H L C G G S L L
1401 CAAGTCAGCC TTCGCTATGA TGGAGCACAC CTCTGTGGGG GATCCCTGCT
    GTTCAGTCGG AAGCGATACT ACCTCGTGTG GAGACACCCC CTAGGGACGA
+3  L S G D W V L T A A H C F P E R N R
1451 CTCCGGGGAC TGGGTGCTGA CAGCCGCCCA CTGCTTCCCG GAGCGGAACC
    GAGGCCCCCTG ACCACGACT GTCGGCGGGT GACGAAGGGC CTCGCCTTGG
+3  R V L S R W R V F A G A V A Q A S
1501 GGGTCCTGTC CCGATGGCGA GTGTTTGCCG GTGCCGTGGC CCAGGCCTCT
    CCCAGGACAG GGCTACCGCT CACAAACGGC CACGGCACCG GGTCCGGAGA
+3  P H G L Q L G V Q A V V Y H G G Y
1551 CCCACGGTC TGCAGCTGGG GGTGCAGGCT GTGGTCTACC ACGGGGGCTA
    GGGGTGCCAG ACGTCGACCC CCACGTCCGA CACCAGATGG TGCCCCGAT
+3  Y L P F R D P N S E E N S N D I A L
1601 TCTTCCCTTT CGGGACCCCA ACAGCGAGGA GAACAGCAAC GATATTGCCC
    AGAAGGGAAA GCCCTGGGGT TGTCGCTCCT CTTGTCGTTG CTATAACGGG
+3  L V H L S S P L P L T E Y I Q P V
1651 TGGTCCACCT CTCCAGTCCC CTGCCCCCTCA CAGAATACAT CCAGCCTGTG
    ACCAGGTGGA GAGGTCAGGG GACGGGGAGT GTCTTATGTA GGTCCGACAC
+3  C L P A A G Q A L V D G K I C T V
1701 TGCCTCCCAG CTGCCGGCCA GGCCCTGGTG GATGGCAAGA TCTGTACCGT
    ACGGAGGGTC GACGGCCGGT CCGGGACCAC CTACCGTTCT AGACATGGCA
+3  V T G W G N T Q Y Y G Q Q A G V L Q
1751 GACGGGCTGG GGCAACACGC AGTACTATGG CCAACAGGCC GGGGTACTCC
    CTGCCCCGACC CCGTTGTGCG TCATGATACC GGTGTCCGG CCCCATGAGG

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FIGURE 9-2

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+3  · Q E A R V P I I S N D V C N G A D
1801 AGGAGGCTCG AGTCCCCATA ATCAGCAATG ATGTCTGCAA TGGCGCTGAT
    TCCTCCGAGC TCAGGGGTAT TAGTCGTTAC TACAGACGTT ACCGCGACTA
+3  · F Y G N Q I K P K M F C A G Y P E ·
1851 TTCTATGGAA ACCAGATCAA GCCCAAGATG TTCTGTGCTG GCTACCCCGA
    AAGATACCTT TGGTCTAGTT CGGGTTCTAC AAGACACGAC CGATGGGGCT
+3  · E G G I D A C Q G D S G G P F V C E
1901 GGGTGGCATT GATGCCTGCC AGGGCGACAG CGGTGGTCCC TTTGTGTGTG
    CCCACCGTAA CTACGGACGG TCCCCTGTGC GCCACCAGGG AAACACACAC
+3  · E D S I S R T P R W R L C G I V S
1951 AGGACAGCAT CTCTCGGACG CCACGTTGGC GGCTGTGTGG CATTGTGAGT
    TCCTGTGCGTA GAGAGCCTGC GGTGCAACCG CCGACACACC GTAACACTCA
+3  · W G T G C A L A Q K P G V Y T K V ·
2001 TGGGGCACTG GCTGTGCCCT GGCCCAAGAAG CCAGGCGTCT ACACCAAAGT
    ACCCCGTGAC CGACACGGGA CCGGGTCTTC GTCCGCAGA TGTGGTTTCA
+3  · V S D F R E W I F Q A I K T H S E A ·
2051 CAGTGA CTTC CGGGAGTGGA TCTTCCAGGC CATAAAGACT CACTCCGAAG
    GTCAGTGAAG GCCCTCACCT AGAAGGTCCG GTATTTCTGA GTGAGGCTTC
+3  · A S G M V T Q L E F G K P I P N P
2101 CCAGCGGCAT GGTGACCCAG CTCGAATTCG GTAAGCCTAT CCCTAACCCCT
    GGTGCGCGTA CCACTGGGTC GAGCTTAAGC CATTCGGATA GGGATTGGGA
+3  · L L G L D S T R T G H H H H H H
2151 CTCTCGGTC TCGATTCTAC GCGTACCGGT CATCATCACC ATCACCATTG
    GAGGAGCCAG AGCTAAGATG CGCATGGCCA GTAGTAGTGG TAGTGGTAAC
2201 AGTTTAAAGC GGCCGCATAG ATAAC TGATC CAGTGTGCTG GAATTAATTC
    TCAAATTTTC CCGGCGTATC TATTGACTAG GTCACACGAC CTTAATTAAG
2251 GCTGTCTGCG AGGGCCAGCT GTTGGGGTGA GTACTCCCTC TCAAAAGCGG
    CGACAGACGC TCCCGGTCGA CAACCCCACT CATGAGGGAG AGTTTTCGCC
2301 GCATGACTTC TGCGCTAAGA TTGTCAAGTTT CCAAAAACGA GGAGGATTTG
    CGTACTGAAG ACGCGATTCT AACAGTCAAA GGTTTTTTGCT CCTCCTAAAC
2351 ATATTCACCT GGCCCGCGGT GATGCCTTTG AGGGTGCCG CGTCCATCTG
    TATAAGTGGA CCGGGCGCCA CTACGGAAC TCCCACCGGC GCAGGTAGAC
2401 GTCAGAAAAG ACAATCTTTT TGTTGTCAAG CTTGAGGTGT GGCAGGCTTG
    CAGTCTTTTC TGTTAGAAA ACAACAGTTC GAACTCCACA CCGTCCGAAC
2451 AGATCTGGCC ATACACTTGA GTGACAATGA CATCCACTTT GCCTTTCTCT
    TCTAGACCGG TATGTGAACT CACTGTTACT GTAGGTGAAA CGGAAAGAGA
2501 CCACAGGTGT CCACTCCCAG GTCCAAC TGC AGGTCGAGCA TGCATCTAGG
    GGTGTCCACA GGTGAGGGTC CAGGTTGACG TCCAGCTCGT ACGTAGATCC
2551 GCGGCCAATT CCGCCCCTCT CCCTCCCCC CCCCTAACGT TACTGGCCGA
    CGCCGGTTAA GGCGGGGAGA GGGAGGGGG GGGGATTGCA ATGACCGGCT
2601 AGCCGCTTGG AATAAGGCCG GTGTGCGTFT GTCTATATGT GATTTTCCAC
    TCGGCGAACC TTATTCCGGC CACACGCAAA CAGATATACA CTAAAAGGTG
2651 CATATTGCCG TCTTTTGGCA ATGTGAGGGC CCGGAAACCT GGCCCTGTCT
    GTATAACGGC AGAAAACCGT TACACTCCCC GGCTTTTGGA CCGGGACAGA
2701 TCTTGACGAG CATTCCTAGG GGTCTTTCCC CTCTCGCCAA AGGAATGCAA
    AGAACTGCTC GTAAGGATCC CCAGAAAGGG GAGAGCGGTT TCCTTACGTT

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FIGURE 9-3

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2751 GGTCTGTTGA ATGTCGTGAA GGAAGCAGTT CCTCTGGAAG CTTCTTGAAG
    CCAGACAAC TACAGCACTT CCTTCGTCAA GGAGACCTTC GAAGAACTTC
2801 ACAAACAACG TCTGTAGCGA CCCTTTGCAG GCAGCGGAAC CCCCACCTG
    TGTTTGTTGC AGACATCGCT GGGAAACGTC CGTCGCCTTG GGGGGTGGAC
2851 GCGACAGGTG CCTCTGCGGC CAAAAGCCAC GTGTATAAGA TACACCTGCA
    CGCTGTCCAC GGAGACGCCG GTTTTCGGTG CACATATTCT ATGTGGACGT
2901 AAGGCGGCAC AACCCAGTG CCACGTTGTG AGTTGGATAG TTGTGGAAAG
    TTCCGCCGTG TTGGGGTCAC GGTGCAACAC TCAACCTATC AACACCTTTC
2951 AGTCAAATGG CTCTCCTCAA GCGTATTCAA CAAGGGGCTG AAGGATGCCC
    TCAGTTTACC GAGAGGAGTT CGCATAAGTT GTTCCCCGAC TTCTACGGG
3001 AGAAGGTACC CCATTGTATG GGATCTGATC TGGGGCCTCG GTGCACATGC
    TCTTCCATGG GGTAACATAC CCTAGACTAG ACCCCGAGC CACGTGTACG
3051 TTTACATGTG TTTAGTCGAG GTTAAAAAAA CGTCTAGGCC CCCCGAACCA
    AAATGTACAC AAATCAGCTC CAATTTTTTT GCAGATCCGG GGGGCTTGGT
3101 CGGGGACGTG GTTTTCCTTT GAAAAACACG ATGATAAGCT TGCCACAACC
    GCCCTGCAC CAAAAGGAAA CTTTTTGTGC TACTATTCTG ACGGTGTTGG
3151 CACAAGGAGA CGACCTTCCA TGACCGAGTA CAAGCCACG GTGCGCCTCG
    GTGTTCCCTCT GCTGGAAGGT ACTGGCTCAT GTTCGGGTGC CACGCGGAGC
3201 CCACCCGCGA CGACGTCCCC CGGGCCGTAC GCACCCTCGC CGCCGCGTTC
    GGTGGGCGCT GCTGCAGGGG GCCCGGCATG CGTGGGAGCG GCGGCGCAAG
3251 GCCGACTACC CCGCCACGCG CCACACCGTC GACCCGGACC GCCACATCGA
    CGGTGATGG GGCAGTGC GCAGGTGGCAG CTGGGCCTGG CGGTGTAGCT
3301 GCGGGTCACC GAGCTGCAAG AACTCTTCCT CACGCGCGTC GGGCTCGACA
    CGCCAGTGG CTCGACGTTT TTGAGAAGGA GTGCGCGCAG CCCGAGCTGT
3351 TCGGCAAGGT GTGGGTCGCG GACGACGGCG CCGCGGTGGC GGTCTGGACC
    AGCCGTTCCA CACCAGCGC CTGCTGCCGC GCGGCCACCG CCAGACCTGG
3401 ACGCCGGAGA GCGTCGAAGC GGGGGCGGTG TTCGCCGAGA TCGGCCCCGCG
    TGCGGCCTCT CGCAGCTTCG CCCC GCCAC AAGCGGCTCT AGCCGGGCGC
3451 CATGGCCGAG TTGAGCGGTT CCGGGCTGGC CGCGCAGCAA CAGATGGAAG
    GTACCGGCTC AACTCGCCAA GGGCCGACCG GCGCGTCGTT GTCTACCTTC
3501 GCCTCCTGGC GCCGCACCGG CCCAAGGAGC CCGCGTGGTT CCTGGCCACC
    CGGAGGACCG CGGCGTGGCC GGGTTCCTCG GCGGCACCAA GGACCGGTGG
3551 GTCGGCGTCT CGCCCGACCA CCAGGGCAAG GGTCTGGGCA GCGCCGTCGT
    CAGCCGACGA GCGGGCTGGT GGTCCTCGTT CCAGACCCGT CGCGGCAGCA
3601 GCTCCCCGGA GTGGAGGCGG CCGAGCGCGC CGGGGTGCCC GCCTTCCTGG
    CGAGGGGCTT CACCTCCGCC GGCTCGCGCG GCCCCACGGG CGGAAGGACC
3651 AGACCTCCGC GCCCGCAAC CTCCCCTTCT ACGAGCGGCT CGGCTTCACC
    TCTGGAGGCG CGGGGCGTTG GAGGGGAAGA TGCTCGCCGA GCCGAAGTGG
3701 GTCACCGCCG ACGTCGAGTG CCCGAAGGAC CGCGCGACCT GGTGCATGAC
    CAGTGGCGGC TGCAGCTCAC GGGCTTCCTG GCGCGCTGGA CCACGTACTG
3751 CCGCAAGCCC GGTGCCTGAC GCGCGCCCCA CGACCCGAG CGCCCGACCG
    GCGCTTCGGG CCACGGACTG CGGGCGGGGT GCTGGGCGTC GCGGGCTGGC
3801 AAAGGAGCGC ACGACCCCAT GGCTCCGACC GAAGCCGACC CGGGCGGGCC
    TTTCTCGCG TGCTGGGGTA CCGAGGCTGG CTTCGGCTGG GCCCGCCGGG
3851 CGCCGACCCC GCACCCGCCC CCGAGGCCCA CCGACTCTAG ACTCGAGATC
    GCGGCTGGGG CGTGGGCGGG GGCTCCGGGT GGCTGAGATC TGAGCTCTAG

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FIGURE 9-4

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3901  GATAATCAAC CTCTGGATTA CAAAATTTGT GAAAGATTGA CTGGTATTCT
      CTATTAGTTG GAGACCTAAT GTTTTAAACA CTTTCTAACT GACCATAAGA
3951  TAACTATGTT GTCCTTTTTA CGCTATGTGG ATACGCTGCT TTAATGCCTT
      ATTGATACAA CGAGGAAAAT GCGATACACC TATGCGACGA AATTACGGAA
4001  TGTATCATGC TATTGCTTCC CGTATGGCTT TCATTTTCTC CTCCTTGTTAT
      ACATAGTACG ATAACGAAGG GCATACCGAA AGTAAAAGAG GAGGAACATA
4051  AAATCCTGGT TGCTGTCTCT TTATGAGGAG TTGTGGCCCG TTGTCAGGCA
      TTTAGGACCA ACGACAGAGA AATACTCCTC AACACCGGGC AACAGTCCGT
4101  ACGTGGCGTG GTGTGCACTG TGTTTGCTGA CGCAACCCCC ACTGGTTGGG
      TGCACCGCAC CACACGTGAC ACAAACGACT GCGTTGGGGG TGACCAACCC
4151  GCATTGCCAC CACCTGTCAG CTCCTTTCCG GGACTTTCGC TTTCCCCCTC
      CGTAACGGTG GTGGACAGTC GAGGAAAGGC CCTGAAAGCG AAAGGGGGAG
4201  CCTATTGCCA CGGCGGAACT CATCGCCGCC TGCCTTGCCC GCTGCTGGAC
      GGATAACGGT GCCGCCTTGA GTAGCGGCGG ACGGAACGGG CGACGACCTG
4251  AGGGGCTCGG CTGTTGGGCA CTGACAATTC CGTGGTGTG TCGGGGAAAT
      TCCCCGAGCC GACAACCCGT GACTGTTAAG GCACCACAAC AGCCCCTTTA
4301  CATCGTCCTT TCCTTGCGTG CTCGCCTGTG TTGCCACCTG GATTCTGCGC
      GTAGCAGGAA AGGAACCGAC GAGCGGACAC AACGGTGGAC CTAAGACGCG
4351  GGGACGTCCT TCTGCTACGT CCCTTCGGCC CTCAATCCAG CGGACCTTCC
      CCCTGCAGGA AGACGATGCA GGGGAAGCCGG GAGTTAGGTC GCCTGGAAGG
4401  TTCCCGCGGC CTGCTGCCGG CTCTGCGGCC TCTTCCGCGT CTTGCGCTTC
      AAGGGCGCCG GACGACGGCC GAGACGCCGG AGAAGGCGCA GAAGCGGAAG
4451  GCCCTCAGAC GAGTCGGATC TCCCTTTGGG CCGCCTCCCC GCCTGATCGA
      CGGGAGTCTG CTCAGCCTAG AGGGAAACCC GCGGAGGGGG CGGACTAGCT
4501  TCTAGAGCTC GCTGATCAGC CTCGACTGTG CCTTCTAGTT GCCAGCCATC
      AGATCTCGAG CGACTAGTCG GAGCTGACAC GGAAGATCAA CGGTGCGTAG
4551  TGTGTGTTGC CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC
      ACAACAAACG GGGAGGGGGC ACGGAAGGAA CTGGGACCTT CCACGGTGAG
4601  CCACTGTCCT TTCTTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT
      GGTGACAGGA AAGGATTATT TTACTCCTTT AACGTAGCGT AACAGACTCA
4651  AGGTGTCATT CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA
      TCCACAGTAA GATAAGACCC CCCACCCAC CCCGTCCTGT CGTTCCCCCT
4701  GGATTGGGAA GACAATAGCA GGCATGCTGG GGATGCGGTG GGCTCTATGG
      CCTAACCCCTT CTGTTATCGT CCGTACGACC CCTACGCCAC CCGAGATACC
4751  CTCTGAGGC GGAAAGAACC AGCTGGGGCT CGAGTGCATT CTAGTTGTGG
      GAAGACTCCG CCTTTCCTTG TCGACCCCGA GCTCACGTAA GATCAACACC
4801  TTTGTCCAAA CTCATCAATG TATCTTATCA TGTCTGTATA CCGTCGACCT
      AAACAGGTTT GAGTAGTTAC ATAGAATAGT ACAGACATAT GGCAGCTGGA
4851  CTAGCTAGAG CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT
      GATCGATCTC GAACCGCATT AGTACCAGTA TCGACAAAGG ACACACTTTA
4901  TGTTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG
      ACAATAGGCG AGTGTTAAGG TGTGTTGTAT GCTCGGCCTT CGTATTTTAC
4951  TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTGC
      ATTTCCGACC CCACGGATTA CTCACTCGAT TGAGTGTAAT TAACGCAACG
5001  GCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATTTA
      CGAGTGACGG GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CGACGTAATT

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FIGURE 9-5

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5051 TGAATCGGCC AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGCGCTCTTC
    ACTTAGCCGG TTGCGCGCCC CTCTCCGCCA AACGCATAAC CCGCGAGAAG
5101 CGCTTCCTCG CTCACTGACT CGCTGCGCTC GGTTCGTTCGG CTGCGGCGAG
    GCGAAGGAGC GAGTGACTGA GCGACGCGAG CCAGCAAGCC GACGCCGCTC
5151 CGGTATCAGC TCACTCAAAG GCGGTAATAC GGT'TATCCAC AGAATCAGGG
    GCCATAGTCG AGTGAGTTTC CGCCATTATG CCAATAGGTG TCTTAGTCCC
5201 GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA
    CTATTGCGTC CTTTCTTGTA CACTCGTTTT CCGGTCGTTT TCCGGTCCTT
5251 CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCCTG
    GGCATTTTTT CGGCGCAACG ACCGCAAAAA GGTATCCGAG GCGGGGGGAC
5301 ACGAGCATCA CAAAAATCGA CGCTCAAGTC AGAGGTGGCG AAACCCGACA
    TGCTCGTAGT GTTTTTAGCT GCGAGTTCAG TCTCCACCGC TTTGGGCTGT
5351 GGA CTATAAA GATACCAGGC GTTTCCTCCCT GGAAGCTCCC TCGTGCGCTC
    CCTGATATTT CTATGGTCCG CAAAGGGGGA CCTTCGAGGG AGCACGCGAG
5401 TCCTGTTC CG ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT
    AGGACAAGGC TGGGACGGCG AATGGCCTAT GGACAGGCGG AAAGAGGGAA
5451 CGGGAAGCGT GGCGCTTTCT CAATGCTCAC GCTGTAGGTA TCTCAGTTCG
    GCCCTTCGCA CCGCGAAAAG GTTACGAGTG CGACATCCAT AGAGTCAAGC
5501 GTGTAGGTCG TTCGCTCCAA GC'TGGGCTGT GTGCACGAAC CCCCCGTTCA
    CACATCCAGC AAGCGAGGTT CGACCCGACA CACGTGCTTG GGGGGCAAGT
5551 GCGCGACCGC TGC GCCTTAT CCGGTA ACTA TCGTCTTGAG TCCAACCCGG
    CGGGCTGGCG ACGCGGAATA GGCCATTGAT AGCAGAACTC AGGTGGGGCC
5601 TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA CAGGATTAGC
    ATTCTGTGCT GAATAGCGGT GACCGTCGTC GGTGACCATT GTCCTAATCG
5651 AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA
    TCTCGCTCCA TACATCCGCC ACGATGTCTC AAGAACTTCA CCACCGGATT
5701 CTACGGCTAC ACTAGAAGGA CAGTATTTGG TATCTGCGCT CTGCTGAAGC
    GATGCCGATG TGATCTTCCT GTCATAAACC ATAGACGCGA GACGACTTCG
5751 CAGTTACCTT CGGAAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC
    GTCAATGGAA GCCTTTTCTT CAACCATCGA GAACTAGGCC GTTTGTTTGG
5801 ACCGCTGGTA GCGGTGGTTT TTTTGTGTTG AAGCAGCAGA TTACGCGCAG
    TGGCGACCAT CGCCACCAA AAAACAAACG TTCGTGCTCT AATGCGCGTC
5851 AAAAAAAGGA TCTCAAGAAG ATCCTTTGAT CTTTTCTACG GGGTCTGACG
    TTTTTTTCCT AGAGTTCTTC TAGGAAACTA GAAAAGATGC CCCAGACTGC
5901 CTCAGTGGAA CGAAAACTCA CGTTAAGGGA TTTTGGTCAT GAGATTATCA
    GAGTCACCTT GCTTTTGAGT GCAATTCCCT AAAACCAGTA CTCTAATAGT
5951 AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC
    TTTTCCTAGA AGTGGATCTA GGAAAATTTA ATTTTACTT CAAAATTTAG
6001 AATCTAAAGT ATATATGAGT AAACCTGGTC TGACAGTTAC CAATGCTTAA
    TTAGATTTCA TATATACTCA TTTGAACCAG ACTGTCAATG GTTACGAATT
6051 TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTTCGTT ATCCATAGTT
    AGTCACTCCG TGGATAGAGT CGCTAGACAG ATAAAGCAAG TAGGTATCAA
6101 GCCTGACTCC CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC
    CGGACTGAGG GGCAGCACAT CTATTGATGC TATGCCCTCC CGAATGGTAG
6151 TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGGCTCCAG
    ACCGGGGTCA CGACGTTACT ATGGCGCTCT GGGTGCGAGT GGCCGAGGTC

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FIGURE 9-6

pIRESpuro2W/hepEK_k

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6201  ATTTATCAGC AATAAACCCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT
      TAAATAGTCG TTATTTGGTC GGTCCGGCCTT CCCGGCTCGC GTCTTCACCA
6251  CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGTT GCCGGAAGC
      GGACGTTGAA ATAGGCGGAG GTAGGTCAGA TAATTAACAA CGGCCCTTCG
6301  TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG
      ATCTCATTCA TCAAGCGGTC AATTATCAAA CGCGTTGCAA CAACGGTAAC
6351  CTACAGGCAT CGTGGTGTCG CGCTCGTCGT TTGGTATGGC TTCATTTCAGC
      GATGTCCGTA GCACCACAGT GCGAGCAGCA AACCATACCG AAGTAAGTCG
6401  TCCGGTTCCC AACGATCAAG GCGAGTTACA TGATCCCCCA TGTTGTGCAA
      AGGCCAAGGG TTGCTAGTTC CGCTCAATGT ACTAGGGGGT ACAACACGTT
6451  AAAAGCGGTT AGCTCCTTCG GTCCCTCCGAT CGTTGTCAGA AGTAAGTTGG
      TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA GCAACAGTCT TCATTCAACC
6501  CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT
      GGCCTCACAA TAGTGAGTAC CAATACCGTC GTGACGTATT AAGAGAATGA
6551  GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTGGTGAGT ACTCAACCAA
      CAGTACGGTA GGCATTCTAC GAAAAGACAC TGACCACTCA TGAGTTGGTT
6601  GTCATTCTGA GAATAGTGTA TCGCGCGACC GAGTTGCTCT TGCCCGGCGT
      CAGTAAGACT CTTATCACAT ACGCCGCTGG CTCAACGAGA ACGGGCCGCA
6651  CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC
      GTTATGCCCT ATTATGGCGC GGTGTATCGT CTTGAAATTT TCACGAGTAG
6701  ATTGGAAAAC GTTCTTCGGG GCGAAAACCTC TCAAGGATCT TACCGCTGTT
      TAACCTTTTG CAAGAAGCCC CGCTTTTGAG AGTTCCTAGA ATGGCGACAA
6751  GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT
      CTCTAGGTCA AGCTACATTG GGTGAGCACG TGGGTTGACT AGAAGTCGTA
6801  CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG AAGGCAAAAT
      GAAAATGAAA GTGGTCGCAA AGACCCACTC GTTTTTGTCC TTCCGTTTTA
6851  GCCGCAAAAA AGGGAATAAG GCGACACGG AAATGTTGAA TACTCATACT
      CGGCGTTTTT TCCCTTATTC CCGCTGTGCC TTTACAACCT ATGAGTATGA
6901  CTTCTTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA
      GAAGGAAAAA GTTATAATAA CTTCGTAAAT AGTCCCAATA ACAGAGTACT
6951  GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG
      CGCCTATGTA TAAACTTACA TAAATCTTTT TATTTGTTTA TCCCAAGGC
7001  CGCACATTTT CCCGAAAAGT GCCACCTGAC GTC
      GCGTGTAAG GGGCTTTTCA CCGTGACTG CAG

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FIGURE 9-7

FIG. 10 (1-12)

pCEP4W/hepEK

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1  TCGAGCGGCC GCTTTAAACT CAATGGTGAT GGTGATGATG ACCGGTACGC
   AGCTCGCCGG CGAAATTTGA GTTACCACTA CCACTACTAC TGGCCATGCG
-3      H H H H H H G T R T
51  GTAGAATCGA GACCGAGGAG AGGGTTAGGG ATAGGCTTAC CGAATTCGAG
   CATCTTAGCT CTGGCTCCTC TCCCAATCCC TATCCGAATG GCTTAAGCTC
-3  ·T S D L G L L P N P I P K G F E L
101 CTGGGTCACC ATGCCGCTGG CTTCCGAGTG AGTCTTTATG GCCTGGAAGA
   GACCCAGTGG TACGGCGACC GAAGCCTCAC TCAGAAATAC CGGACCTTCT
-3  Q T V M G S A E S H T K I A Q F I
151 TCCACTCCCG GAAGTCACTG ACTTTGGTGT AGACGCCTGG CTTCTGGGGC
   AGGTGAGGGC CTTCACTGAC TGAAACCACA TCTGCGGACC GAAGACCCGG
-3  ·I W E R F D S V K T Y V G P K Q A L
201 AGGGCACAGC CAGTGCCCCA ACTCACAATG CCACACAGCC GCCAACGTGG
   TCCCGTGTCTG GTCACGGGGT TGAGTGTTAC GGTGTGTCGG CGGTTGCACC
-3  ·L A C G T G W S V I G C L R W R P
251 CGTCCGAGAG ATGCTGTCTT CACACACAAA GGGACCACCG CTGTCGCCCT
   GCAGGCTCTC TACGACAGGA GTGTGTGTTT CCCTGGTGGC GACAGCGGGA
-3  T R S I S D E C V F P G G S D G Q
301 GGCAGGCATC AATGCCACCC TCGGGGTAGC CAGCACAGAA CATCTTGGGC
   CCGTCCGTAG TTACGGTGGG AGCCCCATCG GTCGTGTCTT GTAGAACCCG
-3  ·Q C A D I G G E P Y G A C F M K P K
351 TTGATCTGGT TTCCATAGAA ATCAGCGCCA TTGCAGACAT CATTGCTGAT
   AACTAGACCA AAGGTATCTT TAGTCGCGGT AACGTCTGTA GTAACGACTA
-3  ·K I Q N G Y F D A G N C V D N S I
401 TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT
   ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA
-3  I P V R A E Q L V G A Q Q G Y Y Q
451 GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC
   CGCACAAACG GGTGCGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG
-3  ·Q T N G W G T V T C I K G D V L A Q
501 TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG
   ACCGGCCGTC GACCCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC
-3  ·Q G A A P L C V P Q I Y E T L P L
551 GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT
   CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA
-3  P S S L H V L A I D N S N E E S N
601 TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC
   ACCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG
-3  ·N P D R F P L Y G G H Y V V A Q V G
651 CCCAGCTGCA GACCGTGGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC
   GGGTCGACGT CTGGCACCCC TCTCCGACC CGGTGCCGTG GCCGTTGTG
-3  ·G L Q L G H P S A Q A V A G A F V
701 TCGCCATCGG GACAGGACCC GGTTCCGCTC CGGGAAGCAG TGGGCGGCTG
   AGCGGTAGCC CTGTCCTGGG CCAAGGCGAG GCCCTTCGTC ACCCGCCGAC
-3  R W R S L V R N R E P F C H A A T

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FIGURE 10-1


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751 TCAGCACCCA GTCCCCGGAG AGCAGGGATC CCCCACAGAG GTGTGCTCCA
    AGTCGTGGGT CAGGGGCCTC TCGTCCCTAG GGGGTGTCTC CACACGAGGT
-3 T L V W D G S L L S G G C L H A G D
801 TCATAGCGAA GGCTGACTTG CCACGGCCAC CGGCCCAAGC TGGTGTCCCG
    AGTATCGCTT CCGACTGAAC GGTGCCGGTG GCCGGGTTCG ACCACAGGGC
-3 D Y R L S V Q W P W R G L S T D R
851 GCCTCCCACG ATCTTGTCGT CGTCGTCCAC GGGCAGCTTC CTGCGGCCAC
    CGGAGGGTGC TAGAACAGCA GCAGCAGGTG CCCGTCAAG GACGCCGGTG
-3 G G V I K D D D D V P L K R R G C
901 AGTCTTGCCA GATGGCGGCC AAGAAACGGC CTC'TGGGGCA ATCACACACG
    TCAGAACCCT CTACCGCCCG TTCTTTGCCG GAGACCCCGT TAGTGTGTGC
-3 C D Q C I A A L F R G R P C D C V S
951 GAGATGACCT CCAGCAGCCT CTGGGTGTGG GGCAGCCTCC CCTCGTCCAC
    CTCTACTGGA GGTCTGTCGA GACCCACACC CCGTCGGAGG GGAGCAGGTG
-3 S I V E L L R Q T H P L R G E D V
1001 ACAGAAGAAG CCCGACGTGC CATTGGCGCC CGCCGTTTCG ACGTCCAGCT
    TGTCTTCTTC GGGCTGCACG GTAACCGCGG GCGGCAAGCG TGCAGGTCTGA
-3 C F F G S T G N A G A T R V D L E
1051 CGGAGTGGGT CAGTGCCCTG AGGAAGCCCA TCTCCTCGCA GCTGAGTCCG
    GCCTCACCCA GTCACGGGAC TCCTTCGGGT AGAGGAGCGT CGACTCAGGC
-3 E S H T L A R L F G M E E C S L G A
1101 GCTACCCTGG CGTTAGAGCG CGAGGAGCAC AGCAGCCGCC ACGTCCCTTC
    CGATGGGACC GCAATCTCGC GCTCCTCGTG TCGTCGGCGG TGCAGGGAAG
-3 A V R A N S R S S C L L R W T G E
1151 CGTCTTGTC AAGACCATGA GCCGAGCGTC CGCAGAGCTG ACCTGCACTG
    GCAGAACAGT TTCTGGTACT CGGCTCGCAG GCGTCTCGAC TGGACGTGAC
-3 T K D F V M L R A D A S S V Q V P
1201 GGTACAGCGG CTCCTGGTCA CTCCTATCCG GAGCGTCACC AGTGGAACCT
    CCATGTCGCC GAGGACCAGT GAGGATAGGC CTCGCACTGG TCACCTTGGA
-3 P Y L P E Q D S R D P A D G T S G P
1251 GGAACCCAGA GCAGCAGTAC CCATAGCAGG AGTGTGTCTG TCTCCATGGT
    CCTTGGGTCT CGTCGTCATG GGTATCGTCC TCACACAGAC AGAGGTACCA
-3 P V W L L L V W L L L T D T E M
1301 GCGATCTGG TACCCAGCTT CTAGAGATCT GACGGTTCAC TAAACGAGCT
    CCGCTAGACC ATGGGTCGAA GATCTCTAGA CTGCCAAGTG ATTTGCTCGA
1351 CTGCTTATAT AGACCTCCA CCGTACACGC CTACCGCCCA TTTGCGTCAA
    GACGAATATA TCTGGAGGGT GGCATGTGCG GATGGCGGGT AAACGCAGTT
1401 CGGGGCGGGG TTATTACGAC ATTTTGGA A GTCCCGTTGA TTTTGGTGCC
    GCCCCGCCCC AATAATGCTG TAAAACCTTT CAGGGCAACT AAAACCACGG
1451 AAAACAAACT CCCATTGACG TCAATGGGGT GGAGACTTGG AAATCCCCGT
    TTTTGTGTTGA GGGTAAGTGC AGTTACCCCA CCTCTGAACC TTTAGGGGCA
1501 GAGTCAAACC GCTATCCACG CCCATTGGTG TACTGCCAAA ACCGCATCAC
    CTCAGTTTGG CGATAGGTGC GGGTAACCAC ATGACGGTTT TGGCGTAGTG
1551 CATGGTAATA GCGATGACTA ATACGTAGAT GTACTGCCAA GTAGGAAAGT
    GTACCATTAT CGCTACTGAT TATGCATCTA CATGACGGTT CATCCTTTCA

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FIGURE 10-2

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1601  CCCGTAAGGT CATGTACTGG GCATAATGCC AGGCGGGCCA TTTACCGTCA
      GGGCATTCCA GTACATGACC CGTATTACGG TCCGCCCCGT AAATGGCAGT
1651  TTGACGTCAA TAGGGGGCGG ACTTGGCATA TGATACACTT GATGTACTGC
      AACTGCAGTT ATCCCCCGCC TGAACCGTAT ACTATGTGAA CTACATGACG
1701  CAAGTGGGCA GTTTACCGTA AATACTCCAC CCATTGACGT CAATGGAAAG
      GTTCACCCGT CAAATGGCAT TTATGAGGTG GGTAAC TGCA GTTACCTTTC
1751  TCCCTATTGG CGTTACTATG GGAACATACG TCATTATTGA CGTCAATGGG
      AGGGATAACC GCAATGATAC CCTTGATATG AGTAATAACT GCAGTTACCC
1801  CGGGGGTTCG TGGGCGGTCA GCCAGGCGGG CCATTTACCG TAAGTTATGT
      GCCCCCAGCA ACCCGCCAGT CGGTCCGCCC GGTAAATGGC ATTCAATACA
1851  AACGCGGAAC TCCATATATG GGCTATGAAC TAATGACCCC GTAATTGATT
      TTGCGCCTTG AGGTATATAC CCGATACTTG ATTACTGGGG CATTAACATA
1901  ACTATTAATA ACTAGTCAAT AATCAATGTC AACATGGCGG TCATATTGGA
      TGATAATTAT TGATCAGTTA TTAGTTACAG TTGTACCGCC AGTATAACCT
1951  CATGAGCCAA TATAAATGTA CATATTATGA TATAGATACA ACGTATGCAA
      GTACTCGGTT ATATTTACAT GTATAATACT ATATCTATGT TGCATACGTT
2001  TGGCCAATAG CCAATATTGA TTTATGCTAT ATAACCAATG ACTAATATGG
      ACCGGTTATC GGTATATACT AAATACGATA TATTGGTTAC TGATTATACC
2051  CTAATTGCCA ATATTGATTC AATGTATAGA TCTTCCATAC CTACCAGTTC
      GATTAACGGT TATAACTAAG TTACATATCT AGAAGGTATG GATGGTCAAG
2101  TGCGCCTGCA GCAATGCAAC AACGTTGCCG GGATCTGCGA TGATAAGCTG
      ACGCGGACGT CGTTACGTTG TTGCAACGGG CCTAGACGCT ACTATTTCGAC
2151  TCAAACATGA GAATTGGTCG ACTAGCTTGG CACGCCAGAA ATCCGCGCGG
      AGTTTGTACT CTTAACCAGC TGATCGAACC GTGCGGTCTT TAGGCGCGCC
2201  TGGTTTTTGG GGGTCGGGGG TGTTTGGCAG CCACAGACGC CCGGTGTTTCG
      ACCAAAAACC CCCAGCCCCC ACAAACCGTC GGTGTCTGCG GGCCACAAGC
2251  TGTCGCGCCA GTACATGCGG TCCATGCCCA GGCCATCAA AAACCATGGG
      ACAGCGCGGT CATGTACGCC AGGTACGGGT CCGGTAGGTT TTTGGTACCC
2301  TCTGTCTGCT CAGTCCAGTC GTGGACCAGA CCCCACGCAA CGCCCCAAAT
      AGACAGACGA GTCAGGTCAG CACCTGGTCT GGGGTGCGTT GCGGGTTTAA
2351  AATAACCCCC ACGAACCATA AACCATTCCC CATGGGGGAC CCCGTCCCTA
      TTATTGGGGG TGCTTGGTAT TTGGTAAGGG GTACCCCTG GGGCAGGGAT
2401  ACCCACGGGG CCAGTGGCTA TGGCAGGGCC TGCCGCCCCG ACGTTGGCTG
      TGGGTGCCCC GGTACCCGAT ACCGTCCCGG ACGGCGGGGC TGCAACCGAC
2451  CGAGCCCTGG GCCTTCACCC GAACCTGGGG GGTGGGGTGG GGAAAAGGAA
      GCTCGGGACC CGGAAGTGGG CTTGAACCCC CCACCCACC CCTTTTCCTT
2501  GAAACGCGGG CGTATTGGCC CCAATGGGGT CTCGGTGGGG TATCGACAGA
      CTTTGCGCCC GCATAACCGG GGTTACCCCA GAGCCACCCC ATAGCTGTCT
2551  GTGCCAGCCC TGGGACCGAA CCCCAGGTTT ATGAACAAAC GACCCAACAC
      CACGGTCGGG ACCCTGGCTT GGGGCGCAAA TACTTGTTTG CTGGGTGTG
2601  CCGTGCGTTT TATTCTGTCT TTTTATTGCC GTCATAGCGC GGGTTCCTTC
      GGCACGCAAA ATAAGACAGA AAAATAACGG CAGTATCGCG CCCAAGGAAG
2651  CCGTATTGTC TCCTTCCGTG TTTCACTTAG CCTCCCCAT CTCCCCATT
      GCCATAACAG AGGAAGGCAC AAAGTCAATC GGAGGGGGTA GAGGGGATAA
2701  CCTTTGCCCT CGGACGAGTG CTGGGGCGTC GGTTCCTACT ATCGGCGAGT
      GGAAACGGGA GCCTGCTCAC GACCCCGCAG CCAAAGGTGA TAGCCGCTCA

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FIGURE 10-3

pCEP4W/hepEK

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2751  ACTTCTACAC AGCCATCGGT CCAGACGGCC GCGCTTCTGC GGGCGATTTG
      TGAAGATGTG TCGGTAGCCA GGTCTGCCGG CGCGAAGACG CCCGCTAAAC
2801  TGTACGCCCCG ACAGTCCCCGG CTCCGGATCG GACGATTGCG TCGCATCGAC
      ACATGCGGGC TGTCAGGGCC GAGGCCTAGC CTGCTAACGC AGCGTAGCTG
2851  CCTGCGCCCA AGCTGCATCA TCGAAAATTGC CGTCAACCAA GCTCTGATAG
      GGACGCGGGT TCGACGTAGT AGCTTTAACG GCAGTTGGTT CGAGACTATC
2901  AGTTGGTCAA GACCAATGCG GAGCATATAC GCCCAGAGCC GCGGCGATCC
      TCAACCAGTT CTGGTTACGC CTCGTATATG CGGGCCTCGG CGCCGCTAGG
2951  TGCAAGCTCC GGATGCCTCC GCTCGAAGTA GCGCGTCTGC TGCTCCATAC
      ACGTTTCGAGG CCTACGAGG CGAGCTTCAT CGCGCAGACG ACGAGGTATG
3001  AAGCCAACCA CGGCCTCCAG AAGAAGATGT TGGCGACCTC GTATTGGGAA
      TTCGGTTGGT GCCGGAGGTC TTCTTCTACA ACCGCTGGAG CATAACCCTT
3051  TCCCCGAACA TCGCCTCGCT CCAGTCAATG ACCGCTGTTA TGCGGCCATT
      AGGGGCTTGT AGCGGAGCGA GGTCAGTTAC TGGCGACAAT ACGCCGGTAA
3101  GTCCGTCAGG ACATTGTTGG AGCCGAAATC CGCGTGCACG AGGTGCCGGA
      CAGGCAGTCC TGTAACAACC TCGGCTTTAG GCGCACGTGC TCCACGGCCT
3151  CTTCGGGGCA GTCCTCGGCC CAAAGCATCA GCTCATCGAG AGCCTGCGCG
      GAAGCCCCGT CAGGAGCCGG GTTTCGTAGT CGAGTAGCTC TCGGACGCGC
3201  ACGGACGCAC TGACGGTGTG GTCCATCACA GTTTGCCAGT GATACACATG
      TGCTGCGTG ACTGCCACAG CAGGTAGTGT CAAACGGTCA CTATGTGTAC
3251  GGGATCAGCA ATCGCGCATA TGAAATCACG CCATGTAGTG TATTGACCGA
      CCCTAGTCGT TAGCGCGTAT ACTTTAGTGC GGTACATCAC ATAACTGGCT
3301  TTCTTGCGG TCCGAATGGG CCGAACCCGC TCGTCTGGCT AAGATCGGCC
      AAGGAACGCC AGGCTTACCC GGCTTGGGCG AGCAGACCGA TTCTAGCCGG
3351  GCAGCGATCG CATCCATGGC CTCCGCGACC GGCTGCAGAA CAGCGGGCAG
      CGTCGCTAGC GTAGGTACCG GAGGCGCTGG CCGACGTCTT GTCGCCCCGC
3401  TTCGGTTTCA GGCAGGTCTT GCAACGTGAC ACCCTGTGCA CGGCGGGAGA
      AAGCCAAAGT CCGTCCAGAA CGTTGCACTG TGGGACACGT GCCGCCCTCT
3451  TGCAATAGGT CAGGCTCTCG CTGAATTCCC CAATGTCAAG CACTTCCGGA
      ACGTTATCCA GTCCGAGAGC GACTTAAGGG GTTACAGTTC GTGAAGGCCCT
3501  ATCGGGAGCG CGGCCGATGC AAAGTGCCGA TAAACATAAC GATCTTTGTA
      TAGCCCTCGC GCCGGCTACG TTTCACGGCT ATTTGTATTG CTAGAAACAT
3551  GAAACCATCG GCGCAGCTAT TTACCCGCAG GACATATCCA CGCCCTCCTA
      CTTTGGTAGC CGCGTCGATA AATGGGCGTC CTGTATAGGT GCGGGAGGAT
3601  CATCGAAGCT GAAAGCACGA GATTCTTCGC CCTCCGAGAG CTGCATCAGG
      GTAGCTTCGA CTTTCGTGCT CTAAGAAGCG GGAGGCTCTC GACGTAGTCC
3651  TCGGAGACGC TGTGCAACTT TTCGATCAGA AACTTCTCGA CAGACGTGCG
      AGCCTCTGCG ACAGCTTGAA AAGCTAGTCT TTGAAGAGCT GTCTGCAGCG
3701  GGTGAGTTCA GGCTTTTTCA TATCTCATTG CCCGGGATCT GCGGCACGCT
      CCACTCAAGT CCGAAAAAGT ATAGAGTAAC GGGCCCTAGA CGCCGTGCGA
3751  GTTGACGCTG TTAAGCGGGT CGCTGCAGGG TCGCTCGGTG TTCGAGGCCA
      CAACTGCGAC AATTGCCCCA GCGACGTCCC AGCGAGCCAC AAGCTCCGGT
3801  CACGCGTCAC CTTAATATGC GAAGTGGACC TGGGACCGCG CCGCCCCGAC
      GTGCGCAGTG GAATTATACG CTTACCTGG ACCCTGGCGC GCGGGGGCTG
3851  TGCATCTGCG TGTTCGAATT CGCCAATGAC AAGACGCTGG GCGGGGTTTG
      ACGTAGACGC ACAAGCTTAA GCGGTTACTG TTCTGCGACC CGCCCCAAAC

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FIGURE 10-4

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3901  TGTCATCATA  GAACTAAAGA  CATGCAAATA  TATTTCTTCC  GGGGACACCG
      ACAGTAGTAT  CTTGATTTCT  GTACGTTTAT  ATAAAGAAGG  CCCCTGTGGC
3951  CCAGCAAACG  CGAGCAACGG  GCCACGGGGA  TGAAGCAGGG  CATGGCGGCC
      GGTTCGTTTG  GCTCGTTGCC  CGGTGCCCCC  ACTTCGTCCC  GTACCGCCGG
4001  GACGCGCTGG  GCTACGTCTT  GCTGGCGTTC  GCGACGCGAG  GCTGGATGGC
      CTGCGCGACC  CGATGCAGAA  CGACCGCAAG  CGCTGCGCTC  CGACCTACCG
4051  CTTCCCCATT  ATGATTCTTC  TCGCTTCCGG  CGGCATCGGG  ATGCCCCGCT
      GAAGGGGTAA  TACTAAGAAG  AGCGAAGGCC  GCCGTAGCCC  TACGGGCGCA
4101  TGCAGGCCAT  GCTGTCCAGG  CAGGTAGATG  ACGACCATCA  GGGACAGCTT
      ACGTCCGGTA  CGACAGGTCC  GTCCATCTAC  TGCTGGTAGT  CCCTGTCGAA
4151  CAAGGATCGC  TCGCGGCTCT  TACCAGCCTA  ACTTCGATCA  CTGGACCGCT
      GTTCCTAGCG  AGCGCCGAGA  ATGGTCGGAT  TGAAGCTAGT  GACCTGGCGA
4201  GATCGTCACG  GCGATTTATG  CCGCCTCGGC  GAGCACATGG  AACGGGTGGG
      CTAGCAGTGC  CGCTAAATAC  GGCGGAGCCG  CTCGTGTACC  TTGCCCAACC
4251  CATGGATTGT  AGGCGCCGCC  CTATACCTTG  TCTGCCCTCC  CGCGTTGCGT
      GTACCTAACA  TCCGCGGCGG  GATATGGAAC  AGACGGAGGG  GCGCAACGCA
4301  CGCGGTGCAT  GGAGCCGGGC  CACCTCGACC  TGAATGGAAG  CCGGCGGCAC
      GCGCCACGTA  CCTCGGCCCG  GTGGAGCTGG  ACTTACCTTC  GGCCGCCGTG
4351  CTCGCTAACG  GATTCACCAC  TCCAAGAATT  GGAGCCAATC  AATTCTTGCG
      GAGCGATTGC  CTAAGTGGTG  AGGTTCTTAA  CCTCGGTTAG  TTAAGAACGC
4401  GAGAACTGTG  AATGCGCAAA  CCAACCCTTG  GCAGAACATA  TCCATCGCGT
      CTCTTGACAC  TTACGCGTTT  GGTTGGGAAC  CGTCTTGAT  AGGTAGCGCA
4451  CCGCCATCTC  CAGCAGCCGC  ACGCGGCGCA  GCAAAAGGCC  AGGAACCGTA
      GGCGGTAGAG  GTCGTGCGCG  TGCGCCGCGT  CGTTTTCCGG  TCCTTGGCAT
4501  AAAAGGCCGC  GTTGCTGGCG  TTTTTCATA  GGCTCCGCCC  CCCTGACGAG
      TTTTCCGGCG  CAACGACCGC  AAAAAGGTAT  CCGAGGCGGG  GGGACTGCTC
4551  CATCACAAAA  ATCGACGCTC  AAGTCAGAGG  TGGCGAAACC  CGACAGGACT
      GTAGTGTTTT  TAGCTGCGAG  TTCAGTCTCC  ACCGCTTTGG  GCTGTCTCTG
4601  ATAAAGATAC  CAGGCGTTTC  CCCCTGGAAG  CTCCCTCGTG  CGCTCTCCTG
      TATTTCTATG  GTCCGCAAAG  GGGGACCTTC  GAGGGAGCAC  GCGAGAGGAC
4651  TTCCGACCTT  GCCGCTTACC  GGATACCTGT  CCGCCTTTCT  CCCTTCGGGA
      AAGGCTGGGA  CGGCGAATGG  CCTATGGACA  GGCGGAAAGA  GGGGAAGCCCT
4701  AGCGTGGCGC  TTTCTCATAG  CTCACGCTGT  AGGTATCTCA  GTTCGGTGTA
      TCGCACCGCG  AAAGAGTATC  GAGTGCAGCA  TCCATAGAGT  CAAGCCACAT
4751  GGTCGTTTCG  TCCAAGCTGG  GCTGTGTGCA  CGAACCCCCC  GTTCAGCCCG
      CCAGCAAGCG  AGGTTCGACC  CGACACACGT  GCTTGGGGGG  CAAGTCGGGC
4801  ACCGCTGCGC  CTTATCCGGT  AACTATCGTC  TTGAGTCCAA  CCCGGTAAGA
      TGGCGACGCG  GAATAGGCCA  TTGATAGCAG  AACTCAGGTT  GGGCCATTCT
4851  CACGACTTAT  CGCCACTGGC  AGCAGCCACT  GGTAACAGGA  TTAGCAGAGC
      GTGCTGAATA  GCGGTGACCG  TCGTCGGTGA  CCATTGTCCT  AATCGTCTCG
4901  GAGGTATGTA  GGCGGTGCTA  CAGAGTTCTT  GAAGTGGTGG  CCTAACTACG
      CTCCATACAT  CCGCCACGAT  GTCTCAAGAA  CTTCAACCACC  GGATTGATGC
4951  GCTACACTAG  AAGGACAGTA  TTTGGTATCT  GCGCTCTGCT  GAAGCCAGTT
      CGATGTGATC  TTCCTGTCAT  AAACCATAGA  CGCGAGACGA  CTTCCGGTCAA
5001  ACCTTCGGAA  AAAGAGTTGG  TAGCTCTTGA  TCCGGCAAAC  AAACCACCGC
      TGGAAGCCTT  TTTCTCAACC  ATCGAGAACT  AGGCCGTTTG  TTTGGTGGCG

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FIGURE 10-5

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5051 TGGTAGCGGT GGTTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA
    ACCATCGCCA CCAAAAAAAC AAACGTTCGT CGTCTAATGC GCGTCTTTTT
5101 AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC TGACGCTCAG
    TTCCTAGAGT TCTTCTAGGA AACTAGAAAA GATGCCCCAG ACTGCGAGTC
5151 TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG
    ACCTTGCTTT TGAGTGCAAT TCCCTAAAAC CAGTACTCTA ATAGTTTTTC
5201 GATCTTCACC TAGATCCTTT TAAATTAATA ATGAAGTTT AAATCAATCT
    CTAGAAGTGG ATCTAGGAAA ATTTAATTTT TACTTCAAAA TTTAGTTAGA
5251 AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG CTTAATCAGT
    TTTTCATATAT ACTCATTTGA ACCAGACTGT CAATGGTTAC GAATTAGTCA
5301 GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA TAGTTGCCTG
    CTCCGTGGAT AGAGTCGCTA GACAGATAAA GCAAGTAGGT ATCAACGGAC
5351 ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC
    TGAGGGGCAG CACATCTATT GATGCTATGC CCTCCCGAAT GGTAGACCGG
5401 CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCAGC TCCAGATTTA
    GGTACGACG TTAATATGGC GCTCTGGGTG CGAGTGGCCG AGGTCTAAAT
5451 TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC
    AGTCGTTATT TGGTCGGTCG GCCTTCCCGG CTCGCGTCTT CACCAGGACG
5501 AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG
    TTGAAATAGG CGGAGGTAGG TCAGATAATT AACAACGGCC CTTGATCTC
5551 TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTGCA
    ATTCATCAAG CGGTCAATTA TCAAACGCGT TGCAACAACG GTAACGACGT
5601 GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG
    CCGTAGCACC ACAGTGCGAG CAGCAAACCA TACCGAAGTA AGTCGAGGCC
5651 TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG
    AAGGGTTGCT AGTTCCGCTC AATGTACTAG GGGGTACAAC ACGTTTTTTC
5701 CGGTTAGCTC CTTCGGTCCT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA
    GCCAATCGAG GAAGCCAGGA GGCTAGCAAC AGTCTTCATT CAACCGGCGT
5751 GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTAATGTCAT
    CACAATAGTG AGTACCAATA CCGTCGTGAC GTATTAAGAG AATGACAGTA
5801 GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT
    CCGTAGGCAT TCTACGAAAA GACACTGACC ACTCATGAGT TGGTTCAGTA
5851 TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC GGCGTCAACA
    AGACTCTTAT CACATACGCC GCTGGCTCAA CGAGAACGGG CCGCAGTTGT
5901 CGGGATAATA CCGCGCCACA TAGCAGAACT TTAAGAGTGC TCATCATTTG
    GCCCTATTAT GGCGCGGTGT ATCGTCTTGA AATTTTCACG AGTAGTAACC
5951 AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT
    TTTTGCAAGA AGCCCCGCTT TTGAGAGTTC CTAGAATGGC GACAACTCTA
6001 CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTTT
    GGTCAAGCTA CATTGGGTGA GCACGTGGGT TGAAGTAAG TCGTAGAAAA
6051 ACTTTACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC
    TGAAAGTGGT CGCAAAGACC CACTCGTTTT TGTCTTCCG TTTTACGGCG
6101 AAAAAAGGGA ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC
    TTTTTTCCCT TATTCCCGCT GTGCCTTTAC AACTTATGAG TATGAGAAGG
6151 TTTTTCATA TTATTGAAGC ATTTATCAGG GTTATTGTCT CATGAGCGGA
    AAAAAGTTAT AATAACTTCG TAAATAGTCC CAATAACAGA GTACTCGCCT

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FIGURE 10-6

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6201 TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG TTCCGCGCAC
    ATGTATAAAC TTACATAAAT CTTTTTATTT GTTTATCCCC AAGGCGCGTG
6251 ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCAT ATTATCATGA
    TAAAGGGGCT TTTCACGGTG GACTGCAGAT TCTTTGGTAA TAATAGTACT
6301 CATTAACTTA TAAAAATAGG CGTATCACGA GGCCCTTTTCG TCTTCAAGAA
    GTAATTGGAT ATTTTTATCC GCATAGTGCT CCGGGAAAGC AGAAGTTCTT
6351 TTCTCATGTT TGACAGCTTA TCATCGATAA GCTGATCCTC ACAGGCCGCA
    AAGAGTACAA ACTGTCTGAAT AGTAGCTATT CGACTAGGAG TGTCCGGCGT
6401 CCCAGCTTTT CTTCCGTTGC CCCAGTAGCA TCTCTGTCTG GTGACCTTGA
    GGGTCGAAAA GAAGGCAACG GGGTCATCGT AGAGACAGAC CACTGGAAC
6451 AGAGGAAGAG GAGGGGTCCC GAGAATCCCC ATCCCTACCG TCCAGCAAAA
    TCTCCTTCTC CTCCCCAGGG CTCTTAGGGG TAGGGATGGC AGGTCGTTTT
6501 AGGGGGACGA GGAATTTGAG GCCTGGCTTG AGGCTCAGGA CGCAAATCTT
    TCCCCCTGCT CCTTAAACTC CGGACCGAAC TCCGAGTCCT GCGTTTAGAA
6551 GAGGATGTTT AGCGGGAGTT TTCCGGGCTG CGAGTAATTG GTGATGAGGA
    CTCCTACAAG TCGCCCTCAA AAGGCCCGAC GCTCATTAAC CACTACTCCT
6601 CGAGGATGGT TCGGAGGATG GGGAATTTTC AGACCTGGAT CTGTCTGACA
    GCTCCTACCA AGCCTCCTAC CCCTTAAAAG TCTGGACCTA GACAGACTGT
6651 GCGACCATGA AGGGGATGAG GGTGGGGGGG CTGTTGGAGG GGGCAGGAGT
    CGCTGGTACT TCCCCTACTC CCACCCCCC GACAACCTCC CCCGTCCTCA
6701 CTGCACTCCC TGTATTCAC T GACGTCGTC TAATAAAGAT GTCTATTGAT
    GACGTGAGGG ACATAAGTGA CTCGCAGCAG ATTATTTCTA CAGATAACTA
6751 CTCTTTTAGT GTGAATCATG TCTGACGAGG GGCCAGGTAC AGGACCTGGA
    GAGAAAATCA CACTTAGTAC AGACTGCTCC CCGGTCCATG TCCTGGACCT
6801 AATGGCCTAG GAGAGAAGGG AGACACATCT GGACCAGAAG GCTCCGGCGG
    TTACCGGATC CTCTCTTCCC TCTGTGTAGA CCTGGTCTTC CGAGGCCGCC
6851 CAGTGGACCT CAAAGAAGAG GGGGTGATAA CCATGGACGA GGACGGGGAA
    GTCACCTGGA GTTCTTCTC CCCCCTATT GGTACCTGCT CCTGCCCCCTT
6901 GAGGACGAGG ACGAGGAGGC GGAAGACCAG GAGCCCCGGG CGGCTCAGGA
    CTCCTGCTCC TGCTCCTCCG CTTCTGCTC CTCGGGGCCC GCCGAGTCCT
6951 TCAGGGCCAA GACATAGAGA TGGTGTCCGG AGACCCCAA AACGTCCAAG
    AGTCCCGGTT CTGTATCTCT ACCACAGGCC TCTGGGGTTT TTGCAGGTTT
7001 TTGCATTGGC TGCAAAGGGA CCCACGGTGG AACAGGAGCA GGAGCAGGAG
    AACGTAACCG ACGTTTCCCT GGGTGCCACC TTGTCTCGT CCTCGTCCTC
7051 CGGGAGGGGC AGGAGCAGGA GGGGCAGGAG CAGGAGGAGG GGCAGGAGCA
    GCCCTCCCCG TCCTCGTCCT CCCCCTCCTC GTCCTCCTCC CCGTCCTCGT
7101 GGAGGAGGGG CAGGAGGGGC AGGAGGGGCA GGAGGGGCAG GAGCAGGAGG
    CCTCCTCCCC GTCTCCTCCG TCCTCCCCGT CCTCCCCGTC CTCGTCTCCT
7151 AGGGGCAGGA GCAGGAGGAG GGGCAGGAGG GGCAGGAGGG GCAGGAGCAG
    TCCCCGTCTC CGTCTCTCTC CCGTCTCTCC CCGTCTCTCC CGTCTCTCTC
7201 GAGGAGGGGC AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG AGCAGGAGGA
    CTCCTCCCCG TCCTCGTCCT CCTCCCCGTC CTCCTCCGTC TCGTCTCTCT
7251 GGGGCAGGAG GGCAGGAGG GGCAGGAGCA GGAGGAGGGG CAGGAGCAGG
    CCCCCTCTCT CCGTCTCTCC CCGTCTCTCGT CCTCTCTCCC GTCTCTCTCT
7301 AGGAGGGGCA GGAGGGGCAG GAGCAGGAGG AGGGGCAGGA GGGGCAGGAG
    TCCTCCCCGT CCTCCCCGTC CTCGTCTCTC TCCCCGTCTC CCCCCTCTCT

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FIGURE 10-7

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7351  GGGCAGGAGC AGGAGGAGGG GCAGGAGCAG GAGGGGCAGG AGGGGCAGGA
      CCCGTCCTCG TCCTCCTCCC CGTCCTCGTC CTCCCCGTCC TCCCCGTCC
7401  GGGGCAGGAG CAGGAGGGGC AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG
      CCCCCGTCTC GTCCTCCCCG TCCTCGTCCT CCTCCCCGTC CTCCCCGTCC
7451  AGGGGCAGGA GCAGGAGGGG CAGGAGCAGG AGGGGCAGGA GCAGGAGGGG
      TCCCCGTCTC CGTCCTCCCC GTCTCTCGTC TCCCCGTCTC CGTCCTCCCC
7501  CAGGAGCAGG AGGGGCAGGA GGGGCAGGAG CAGGAGGGGC AGGAGGGGCA
      GTCTCTCGTC TCCCCGTCTC CCCCCGTCTC GTCTTCCCCG TCCTCCCCGT
7551  GGAGCAGGAG GGGCAGGAGG GGCAGGAGCA GGAGGAGGGG CAGGAGGGGC
      CCTCGTCCTC CCCGTCCTCC CCGTCCTCGT CCTCCTCCCC GTCTTCCCCG
7601  AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG AGCAGGAGGG GCAGGAGGGG
      TCCTCGTCCT CCTCCCCGTC CTCCCCGTCC TCGTCCTCCC CGTCCTCCCC
7651  CAGGAGCAGG AGGGGCAGGA GGGGCAGGAG CAGGAGGGGC AGGAGGGGCA
      GTCTCTCGTC TCCCCGTCTC CCCCCGTCTC GTCTTCCCCG TCCTCCCCGT
7701  GGAGCAGGAG GAGGGGCAGG AGCAGGAGGG GCAGGAGCAG GAGGTGGAGG
      CCTCGTCCTC CTCCCCGTCC TCGTCCTCCC CGTCCTCGTC CTCCACCTCC
7751  CCGGGGTCGA GGAGGCAGTG GAGGCCGGGG TCGAGGAGGT AGTGGAGGCC
      GGCCCCAGCT CCTCCGTCAC CTCCGGCCCC AGCTCCTCCA TCACCTCCGG
7801  GGGGTCGAGG AGGTAGTGGA GGCCGCCGGG GTAGAGGACG TGAAAGAGCC
      CCCCAGCTCC TCCATCACCT CCGGCGGCCC CATCTCCTGC ACTTCTCGG
7851  AGGGGGGGAA GTCGTGAAAG AGCCAGGGGG AGAGGTCGTG GACGTGGAGA
      TCCCCCCTT CAGCACTTTC TCGGTCCCCC TCTCCAGCAC CTGCACCTCT
7901  AAAGAGGCCC AGGAGTCCCA GTAGTCAGTC ATCATCATCC GGTCTCCAC
      TTTCTCCGGG TCCTCAGGGT CATCAGTCAG TAGTAGTAGG CCCAGAGGTG
7951  CGCGCAGGCC CCCTCCAGGT AGAAGGCCAT TTTTCCACCC TGTAGGGGAA
      GCGCGTCCGG GGGAGGTCCA TCTTCCGGTA AAAAGGTGGG ACATCCCCCT
8001  GCCGATTATT TTGAATACCA CCAAGAAGGT GGCCAGATG GTGAGCCTGA
      CGGCTAATAA AACTTATGGT GGTTCTTCCA CCGGGTCTAC CACTCGGACT
8051  CGTGCCCCCG GGAGCGATAG AGCAGGGCCC CGCAGATGAC CCAGGAGAAG
      GCACGGGGGC CCTCGCTATC TCGTCCCGGG GCGTCTACTG GGTCTCTTC
8101  GCCCAAGCAC TGGACCCCGG GGTCAGGGTG ATGGAGGCAG GCGCAAAAAA
      CGGGTTCGTG ACCTGGGGCC CCAGTCCAC TACCTCCGTC CGCGTTTTTT
8151  GGAGGGTGGT TTGGAAAGCA TCGTGGTCAA GGAGGTCCA ACCCGAAATT
      CCTCCCACCA AACCTTTCGT AGCACCAGTT CCTCCAAGGT TGGGCTTTAA
8201  TGAGAACATT GCAGAAGGTT TAAGAGCTCT CCTGGCTAGG AGTCACGTAG
      ACTCTTGTA AACTTTCCTT TCTCTGAGA GGACCGATCC TCAGTGCATC
8251  AAAGGACTAC CGACGAAGGA ACTTGGGTCG CCGGTGTGTT CGTATATGGA
      TTTCTTGATG GCTGCTTCCT TGAACCCAGC GGCCACACAA GCATATACCT
8301  GGTAAGTAAGA CCTCCCTTTA CAACCTAAGG CGAGGAACTG CCCTTGCTAT
      CCATCATCTT GGAGGGAAAT GTTGGATTCC GCTCCTTGAC GGGAACGATA
8351  TCCACAATGT CGTCTTACAC CATTGAGTCG TCTCCCCTTT GGAATGGCCC
      AGGTGTTACA GCAGAATGTG GTAACCTCAGC AGAGGGGAAA CCTTACCGGG
8401  CTGGACCCCG CCCACAACCT GGCCCGCTAA GGGAGTCCAT TGTCTGTTAT
      GACCTGGGCC GGGTGTGGGA CCGGGCGATT CCCTCAGGTA ACAGACAATA
8451  TTCATGGTCT TTTTACAAAC TCATATATTT GCTGAGGTTT TGAAGGATGC
      AAGTACCAGA AAAATGTTTG AGTATATAAA CGACTCCAAA ACTTCCTACG

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FIGURE 10-8

8501	GATTAAGGAC	CTTGTTATGA	CAAAGCCCCG	TCCTACCTGC	AATATCAGGG
	CTAATTCCCTG	GAACAATACT	GTTTCGGGCG	AGGATGGACG	TTATAGTCCC
8551	TGACTGTGTG	CAGCTTTGAC	GATGGAGTAG	ATTTGCCTCC	CTGGTTTCCA
	ACTGACACAC	GTCGAAACTG	CTACCTCATC	TAAACGGAGG	GACCAAAGGT
8601	CCTATGGTGG	AAGGGGCTGC	CGCGGAGGGT	GATGACGGAG	ATGACGGAGA
	GGATAACCAC	TTCCCCGACG	GCGCCTCCCA	CTACTGCCTC	TACTGCCTCT
8651	TGAAGGAGGT	GATGGAGATG	AGGGTGAGGA	AGGGCAGGAG	TGATGTAACT
	ACTTCCTCCA	CTACCTCTAC	TCCCACTCCT	TCCCGTCCTC	ACTACATTGA
8701	TGTTAGGAGA	CGCCCTCAAT	CGTATTAAAA	GCCGTGTATT	CCCCGCACT
	ACAATCCTCT	GCGGGAGTTA	GCATAATTTT	CGGCACATAA	GGGGGCGTGA
8751	AAAGAATAAA	TCCCCAGTAG	ACATCATGCG	TGCTGTTGGT	GTATTTCTGG
	TTTCTTATTT	AGGGGTCATC	TGTAGTACGC	ACGACAACCA	CATAAAGACC
8801	CCATCTGTCT	TGTCACCATT	TTCGTCTCCT	CAACATGGGG	CAATTGGGCA
	GGTAGACAGA	ACAGTGGTAA	AAGCAGGAGG	GTTGTACCCC	GTTAACCCGT
8851	TACCCATGTT	GTCACGTCAC	TCAGCTCCGC	GCTCAACACC	TTCTCGCGTT
	ATGGGTACAA	CAGTGCAGTG	AGTCGAGGCG	CGAGTTGTGG	AAGAGCGCAA
8901	GGAAAACATT	AGCGACATTT	ACCTGGTGAG	CAATCAGACA	TGCGACGGCT
	CCTTTTGTAA	TCGCTGTAAA	TGGACCACTC	GTTAGTCTGT	ACGCTGCCGA
8951	TTAGCCTGGC	CTCCTTAAAT	TCACCTAAGA	ATGGGAGCAA	CCAGCATGCA
	AATCGGACCG	GAGGAATTTA	AGTGGATTCT	TACCCTCGTT	GGTCGTACGT
9001	GGAAAAGGAC	AAGCAGCGAA	AATTCACGCC	CCCTTGGGAG	GTGGCGGCAT
	CCTTTTCCTG	TTCGTCGCTT	TTAAGTGCGG	GGGAACCCCTC	CACCGCCGTA
9051	ATGCAAAGGA	TAGCACTCCC	ACTCTACTAC	TGGGTATCAT	ATGCTGACTG
	TACGTTTCCT	ATCGTGAGGG	TGAGATGATG	ACCCATAGTA	TACGACTGAC
9101	TATATGCATG	AGGATAGCAT	ATGCTACCCG	GATACAGATT	AGGATAGCAT
	ATATACGTAC	TCCTATCGTA	TACGATGGGC	CTATGTCTAA	TCCTATCGTA
9151	ATACTACCCA	GATATAGATT	AGGATAGCAT	ATGCTACCCA	GATATAGATT
	TATGATGGGT	CTATATCTAA	TCCTATCGTA	TACGATGGGT	CTATATCTAA
9201	AGGATAGCCT	ATGCTACCCA	GATATAAATT	AGGATAGCAT	ATACTACCCA
	TCCTATCGGA	TACGATGGGT	CTATATTTAA	TCCTATCGTA	TATGATGGGT
9251	GATATAGATT	AGGATAGCAT	ATGCTACCCA	GATATAGATT	AGGATAGCCT
	CTATATCTAA	TCCTATCGTA	TACGATGGGT	CTATATCTAA	TCCTATCGGA
9301	ATGCTACCCA	GATATAGATT	AGGATAGCAT	ATGCTACCCA	GATATAGATT
	TACGATGGGT	CTATATCTAA	TCCTATCGTA	TACGATGGGT	CTATATCTAA
9351	AGGATAGCAT	ATGCTATCCA	GATATTTGGG	TAGTATATGC	TACCCAGATA
	TCCTATCGTA	TACGATAGGT	CTATAAACCC	ATCATATACG	ATGGGTCTAT
9401	TAAATTAGGA	TAGCATATAC	TACCCTAATC	TCTATTAGGA	TAGCATATGC
	ATTTAATCCT	ATCGTATATG	ATGGGATTAG	AGATAATCCT	ATCGTATACG
9451	TACCCGGATA	CAGATTAGGA	TAGCATATAC	TACCCAGATA	TAGATTAGGA
	ATGGGCCCTAT	GTCTAATCCT	ATCGTATATG	ATGGGTCTAT	ATCTAATCCT
9501	TAGCATATGC	TACCCAGATA	TAGATTAGGA	TAGCCTATGC	TACCCAGATA
	ATCGTATACG	ATGGGTCTAT	ATCTAATCCT	ATCGGATACG	ATGGGTCTAT
9551	TAAATTAGGA	TAGCATATAC	TACCCAGATA	TAGATTAGGA	TAGCATATGC
	ATTTAATCCT	ATCGTATATG	ATGGGTCTAT	ATCTAATCCT	ATCGTATACG
9601	TACCCAGATA	TAGATTAGGA	TAGCCTATGC	TACCCAGATA	TAGATTAGGA
	ATGGGTCTAT	ATCTAATCCT	ATCGGATACG	ATGGGTCTAT	ATCTAATCCT

FIGURE 10-9

pCEP4w/hepEK

9651	TAGCATATGC	TATCCAGATA	TTTGGGTTAGT	ATATGCTACC	CATGGCAACA
	ATCGTATACG	ATAGGTCTAT	AAACCCATCA	TATACGATGG	GTACCGTTGT
9701	TTAGCCCACC	GTGCTCTCAG	CGACCTCGTG	AATATGAGGA	CCAACAACCC
	AATCGGGTGG	CACGAGAGTC	GCTGGAGCAC	TTATACTCCT	GGTTGTTGGG
9751	TGTGCTTGGC	GCTCAGGCGC	AAGTGTGTGT	AATTTGTCCT	CCAGATCGCA
	ACACGAACCG	CGAGTCCGCG	TTCACACACA	TTAAACAGGA	GGTCTAGCGT
9801	GCAATCGCGC	CCCTATCTTG	GCCCCGCCAC	CTACTTATGC	AGGTATTCCC
	CGTTAGCGCG	GGGATAGAAC	CGGGCGGGTG	GATGAATACG	TCCATAAGGG
9851	CGGGGTGCCA	TTAGTGTTT	TGTGGGCAAG	TGGTTTGACC	GCAGTGGTTA
	GCCCCACGGT	AATCACCAAA	ACACCCGTTT	ACCAAACCTG	CGTCACCAAT
9901	GCGGGGTTAC	AATCAGCCAA	GTTATTACAC	CCTTATTTTA	CAGTCCAAAA
	CGCCCCAATG	TTAGTCGGTT	CAATAATGTG	GGAATAAAAT	GTCAGGTTTT
9951	CCGCAGGGCG	GCGTGTGGGG	GCTGACGCGT	GCCCCCACTC	CACAATTTCA
	GGCGTCCCGC	CGCACACCCC	CGACTGCGCA	CGGGGGTGAG	GTGTTAAAGT
10001	AAAAAAGAG	TGGCCACTTG	TCTTTGTTTA	TGGGCCCCAT	TGGCGTGGAG
	TTTTTTTCTC	ACCGGTGAAC	AGAAACAAAT	ACCCGGGGTA	ACCGCACCTC
10051	CCCCGTTTAA	TTTTCGGGGG	TGTTAGAGAC	AACCAGTGGA	GTCCGCTGCT
	GGGGCAAATT	AAAAGCCCCC	ACAATCTCTG	TTGGTCACCT	CAGGCGACGA
10101	GTCGGCGTCC	ACTCTCTTTC	CCCTTGTTAC	AAATAGAGTG	TAACAACATG
	CAGCCGCAGG	TGAGAGAAAG	GGGAACAATG	TTTATCTCAC	ATTGTTGTAC
10151	GTTACACTGT	CTTGGTCCCT	GCCTGGGACA	CATCTTAATA	ACCCCAAGTAT
	CAAGTGGACA	GAACCAGGGA	CGGACCCTGT	GTAGAATTAT	TGGGGTCATA
10201	CATATTGCAC	TAGGATTATG	TGTTGCCCCAT	AGCCATAAAT	TCGTGTGAGA
	GTATAACGTG	ATCCTAATAC	ACAACGGGTA	TCGGTATTTA	AGCACACTCT
10251	TGGACATCCA	GTCTTTACGG	CTTGTCCTCA	CCCCATGGAT	TTCTATTGTT
	ACCTGTAGGT	CAGAAATGCC	GAACAGGGGT	GGGGTACCTA	AAGATAACAA
10301	AAAGATATTC	AGAATGTTTC	ATTCTTACAC	TAGTATTTAT	TGCCCCAGGG
	TTTCTATAAG	TCTTACAAAG	TAAGGATGTG	ATCATAAATA	ACGGGTTCCT
10351	GTTTGTGAGG	GTTATATTGG	TGTCATAGCA	CAATGCCACC	ACTGAACCCC
	CAAACACTCC	CAATATAACC	ACAGTATCGT	GTTACGGTGG	TGACTTGGGG
10401	CCGTCCAAAT	TTTATTCTGG	GGGCGTCACC	TGAAACCTTG	TTTTCGAGCA
	GGCAGGTTTA	AAATAAGACC	CCCAGTGGG	ACTTTGGAAC	AAAAGCTCGT
10451	CCTCACATAC	ACCTTACTGT	TCACAACCTA	GCAGTTATTC	TATTAGCTAA
	GGAGTGTATG	TGGAATGACA	AGTGTGAGT	CGTCAATAAG	ATAATCGATT
10501	ACGAAGGAGA	ATGAAGAAGC	AGGCGAAGAT	TCAGGAGAGT	TCACTGCCCCG
	TGCTTCCTCT	TACTTCTTCG	TCCGCTTCTA	AGTCCTCTCA	AGTGACGGGC
10551	CTCCTTGATC	TTCAGCCACT	GCCCTTGTTA	CTAAAATGGT	TCACTACCCCT
	GAGGAACCTAG	AAGTCGGTGA	CGGGAACACT	GATTTTACCA	AGTGATGGGA
10601	CGTGGAATCC	TGACCCCATG	TAAATAAAAC	CGTGACAGCT	CATGGGGTGG
	GCACCTTAGG	ACTGGGGTAC	ATTTATTTTG	GCACTGTCTG	GTACCCCAAC
10651	GAGATATCGC	TGTTCTTTAG	GACCCTTTTA	CTAACCCCTA	TTCGATAGCA
	CTCTATAGCG	ACAAGGAATC	CTGGGAAAAT	GATTGGGATT	AAGCTATCGT
10701	TATGCTTCCC	GTTGGGTAAAC	ATATGCTATT	GAATTAGGGT	TAGTCTGGAT
	ATACGAAGGG	CAACCCATTG	TATACGATAA	CTTAATCCCA	ATCAGACCTA
10751	AGTATATACT	ACTACCCGGG	AAGCATATGC	TACCCGTTTA	GGGTAAACAA
	TCATATATGA	TGATGGGCC	TTCTGATACG	ATGGGCAAAT	CCCAATTGTT

FIGURE 10-10

pCEP4W/hepEK

10801	GGGGGCCTTA	TAAACACTAT	TGCTAATGCC	CTCTTGAGGG	TCCGCTTATC
	CCCCCGGAAT	ATTTGTGATA	ACGATTACGG	GAGAACTCCC	AGGCGAATAG
10851	GGTAGCTACA	CAGGCCCTTC	TGATTGACGT	TGGTGTAGCC	TCCCGTAGTC
	CCATCGATGT	GTCCGGGGAG	ACTAACTGCA	ACCACATCGG	AGGGCATCAG
10901	TTCCTGGGCC	CCTGGGAGGT	ACATGTCCCC	CAGCATTGGT	GTAAGAGCTT
	AAGGACCCGG	GGACCCTCCA	TGTACAGGGG	GTCGTAACCA	CATTCTCGAA
10951	CAGCCAAGAG	TTACACATAA	AGGCAATGTT	GTGTTGCAGT	CCACAGACTG
	GTCGGTTCTC	AATGTGTATT	TCCGTTACAA	CACAACGTCA	GGTGTCTGAC
11001	CAAAGTCTGC	TCCAGGATGA	AAGCCACTCA	GTGTTGGCAA	ATGTGCACAT
	GTTTCAGACG	AGGTCCTACT	TTCGGTGAGT	CACAACCGTT	TACACGTGTA
11051	CCATTTATAA	GGATGTCAAC	TACAGTCAGA	GAACCCCTTT	GTGTTTGGTC
	GGTAAATATT	CCTACAGTTG	ATGTCAGTCT	CTTGGGGAAA	CACAAACCAG
11101	CCCCCCCCGTG	TCACATGTGG	AACAGGGCCC	AGTTGGCAAG	TTGTACCAAC
	GGGGGGGCAC	AGTGTACACC	TTGTCCCGGG	TCAACCGTTC	AACATGGTTG
11151	CAACTGAAGG	GATTACATGC	ACTGCCCCGC	GAAGAAGGGG	CAGAGATGCC
	GTTGACTTCC	CTAATGTACG	TGACGGGGCG	CTTCTTCCCC	GTCTCTACGG
11201	GTAGTCAGGT	TTAGTTCGTC	CGGCGGCGGG	GCTCTAGAGT	CGACCGGTCA
	CATCAGTCCA	AATCAAGCAG	GCCGCCGCC	CGAGATCTCA	GCTGGCCAGT
11251	TGGCTGCGCC	CCGACACCCG	CCAACACCCG	CTGACGCGCC	CTGACGGGCT
	ACCGACGCGG	GGCTGTGGGC	GGTTGTGGGC	GAATGCGCGG	GAATGCCCCA
11301	TGTCTGCTCC	CGGCATCCGC	TTACAGACAA	GCTGTGACCG	TCTCCGGGAG
	ACAGACGAGG	GCCGTAGGCG	AATGTCTGTT	CGACACTGGC	AGAGGCCCTC
11351	CTGCATGTGT	CAGAGGTTTT	CACCGTCATC	ACCGAAACGC	GCGAGGCAGC
	GACGTACACA	GTCTCCAAAA	GTGGCAGTAG	TGGCTTTGCG	CGCTCCGTCG
11401	CGGATCATAA	TCAGCCATAC	CACATTTGTA	GAGGTTTTAC	TTGCTTTAAA
	GCCTAGTATT	AGTCGGTATG	GTGTAAACAT	CTCCAAAATG	AACGAAATTT
11451	AAACCTCCCC	ACCTCCCCCT	GAACCTGAAA	CATAAAATGA	ATGCAATTGT
	TTTGAGAGGG	TGGAGGGGGA	CTTGGACTTT	GTATTTTACT	TACGTTAACA
11501	TGTTGTTAAC	TTGTTTATTG	CAGCTTATAA	TGGTTACAAA	TAAAGCAATA
	ACAACAATTG	AACAAATAAC	GTGCAATATT	ACCAATGTTT	ATTTTCGTTAT
11551	GCATCACAAA	TTTCACAAAT	AAAGCATTTT	TTTCACTGCA	TTCTAGTTGT
	CGTAGTGTTT	AAAGTGTTTA	TTTCGTAAAA	AAAGTGACGT	AAGATCAACA
11601	GGTTTGTCCA	AACTCATCAA	TGTATCTTAT	CATGTCTGGA	TCCCACGTGC
	CCAAACAGGT	TTGAGTAGTT	ACATAGAATA	GTACAGACCT	AGGGTGCACG
11651	AGGCGGGGAG	GCGGCCCAAA	GGGAGATCCG	ACTCGTCTGA	GGGCGAAGGC
	TCCGCCCCCTC	CGCCGGGTTT	CCCTCTAGGC	TGAGCAGACT	CCCCTTCCG
11701	GAAGACGCGG	AAGAGGCCGC	AGAGCCGGCA	GCAGGCCGCG	GGAAGGAAGG
	CTTCTGCGCC	TTCTCCGGCG	TCTCGGCCGT	CGTCCGGCGC	CCTTCCTTCC
11751	TCCGCTGGAT	TGAGGGCCGA	AGGGACGTAG	CAGAAGGACG	TCCCGCGCAG
	AGGCGACCTA	ACTCCCGGCT	TCCCTGCATC	GTCTTCCTGC	AGGGCGCGTC
11801	AATCCAGGTG	GCAACACAGG	CGAGCAGCCA	AGGAAAGGAC	GATGATTTCC
	TTAGGTCCAC	CGTTGTGTCC	GCTCGTCGGT	TCCTTTCCCTG	CTACTAAAGG
11851	CCGACAACAC	CACGGAATTG	TCAGTGCCCA	ACAGCCGAGC	CCCTGTCCAG
	GGCTGTTGTG	GTGCCTTAAC	AGTCACGGGT	TGTCGGCTCG	GGGACAGGTC
11901	CAGCGGGCAA	GGCAGGCGGC	GATGAGTTCC	GCCGTGGCAA	TAGGGAGGGG
	GTCGCCCCGT	CCGTCCGCCG	CTACTCAAGG	CGGCACCGTT	ATCCCTCCCC

FIGURE 10-11

pCEP4W/hepEK

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11951  GAAAGCGAAA GTCCCGGAAA GGAGCTGACA GGTGGTGGCA ATGCCCCAAC
      CTTTCGCTTT CAGGGCCTTT CCTCGACTGT CCACCACCGT TACGGGGTTG
12001  CAGTGGGGGT TCGTCAGCA AACACAGTGC ACACCACGCC ACGTTGCCTG
      GTCACCCCCA ACGCAGTCGT TTGTGTCACG TGTGGTGCGG TGCAACGGAC
12051  ACAACGGGCC ACAACTCCTC ATAAAGAGAC AGCAACCAGG ATTTATACAA
      TGTTGCCCGG TGTTGAGGAG TATTTCTCTG TCGTTGGTCC TAAATATGTT
12101  GGAGGAGAAA ATGAAAGCCA TACGGGAAGC AATAGCATGA TACAAAGGCA
      CCTCCTCTTT TACTTTCGGT ATGCCCTTCG TTATCGTACT ATGTTTCCGT
12151  TTAAAGCAGC GTATCCACAT AGCGTAAAAG GAGCAACATA GTTAAGAATA
      AATTTTCGTCG CATAGGTGTA TCGCATTTTC CTCGTTGTAT CAATTCTTAT
12201  CCAGTCAATC TTTCACAAAT TTTGTAATCC AGAGGTTGAT TC
      GGTCAAGTTAG AAAGTGTTTA AAACATTAGG TCTCCAATA AG

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FIGURE 10-12

FIG 11 (1-17)

pCEP4W/hep36

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1  TCGAGCGGCC GCTTTAACT CAATGGTGAT GGTGATGATG ACCGGTACGC
   AGCTCGCCGG CGAAATTTGA GTTACCACTA CCACTACTAC TGGCCATGCG
-3      H H H H H H G T R T
51  GTAGAATCGA GACCGAGGAG AGGGTTAGGG ATAGGCTTAC CGAATTCGAG
   CATCTTAGCT CTGGCTCCTC TCCCAATCCC TATCCGAATG GCTTAAGCTC
-3  ·T S D L G L L P N P I P K G F E L
101 CTGGGTCACC ATGCCGCTGG CTTCGGAGTG AGTCTTTATG GCCTGGAAGA
   GACCCAGTGG TACGGCGACC GAAGCCTCAC TCAGAAATAC CGGACCTTCT
-3  Q T V M G S A E S H T K I A Q F I
151 TCCACTCCCG GAAGTCACTG ACTTTGGTGT AGACGCCTGG CTTCTGGGCC
   AGGTGAGGGC CTTCAGTGAC TGAAACCACA TCTGCGGACC GAAGACCCGG
-3  ·I W E R F D S V K T Y V G P K Q A L
201 AGGGCACAGC CAGTGCCCCA ACTCACAATG CCACACAGCC GCCAACGTGG
   TCCCGTGTGC GTACGCGGGT TGAGTGTTAC GGTGTGTCCG CGGTTGCACC
-3  ·L A C G T G W S V I G C L R W R P
251 CGTCCGAGAG ATGCTGTCCT CACACACAAA GGGACCACCG CTGTGCCCCCT
   GCAGGCTCTC TACGACAGGA GTGTGTGTTT CCCTGGTGGC GACAGCGGGA
-3  T R S I S D E C V F P G G S D G Q
301 GGCAGGCATC AATGCCACCC TCGGGGTAGC CAGCACAGAA CATCTTGGGC
   CCGTCCGTAG TTACGGTGGG AGCCCCATCG GTCGTGTCTT GTAGAACCCG
-3  ·Q C A D I G G E P Y G A C F M K P K
351 TTGATCTGGT TTCCATAGAA ATCAGCGCCA TTGCAGACAT CATTGCTGAT
   AACTAGACCA AAGGTATCTT TAGTCGCGGT AACGTCTGTA GTAACGACTA
-3  ·K I Q N G Y F D A G N C V D N S I
401 TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT
   ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA
-3  I P V R A E Q L V G A Q Q G Y Y Q
451 GCGTGTGTC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC
   CGCACAAACG GGTGCGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG
-3  ·Q T N G W G T V T C I K G D V L A Q
501 TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCGAG
   ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC
-3  ·Q G A A P L C V P Q I Y E T L P L
551 GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT
   CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA
-3  P S S L H V L A I D N S N E E S N
601 TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAAGACAC AGCCTGCACC
   ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG
-3  ·N P D R F P L Y G G H Y V V A Q V G
651 CCCAGCTGCA GACCGTGGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC
   GGGTCGACGT CTGGCACCCC TCTCCGGACC CGGTGCCGTG GCCGTTGTG
-3  ·G L Q L G H P S A Q A V A G A F V
701 TCGCCATCGG GACAGGACCC GGTTCCGCTC CGGGAAGCAG TGGGCGGCTG
   AGCGGTAGCC CTGTCTTGGG CCAAGGCGAG GCCCTTCGTC ACCCGCCGAC
-3  R W R S L V R N R E P F C H A A T

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FIGURE 11-1

Fig 11

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751 TCAGCACCCA GTCCCCGGAG AGCAGGGATC CCCCACAGAG GTGTGCTCCA
    AGTCGTGGGT CAGGGGCCTC TCGTCCCTAG GGGGTGTCTC CACACGAGGT
-3 T L V W D G S L L S G G C L H A G D
801 TCATAGCGAA GGCTGACTTG CCACGGCCAC CGGCCCAAGC TGGTGTCCCG
    AGTATCGCTT CCGACTGAAC GGTGCCCGTG GCCGGGTTCG ACCACAGGGC
-3 D Y R L S V Q W P W R G L S T D R
851 GCCTCCACAG ATCTTGTCGT CGTCGTCCAC GGGCAGCTTC CTGCGGCCAC
    CGGAGGGTGC TAGAACAGCA GCAGCAGGTG CCCGTCAAG GACGCCGGTG
-3 G G V I K D D D D V P L K R R G C
901 AGTCTTGGTC CGGAGCGTCA CCAGTGGAAC CTGGAACCCA GAGCAGCAGT
    TCAGAACCAAG GCCTCGCAGT GGTACCTTG GACCTTGGGT CTCGTCTGTC
-3 C D Q D P A D G T S G P V W L L L V
951 ACCCATAGCA GGAGTGTGTC TGTCTCCATG GTGGCGATCT GGTACCCAGC
    TGGGTATCGT CCTCACACAG ACAGAGGTAC CACCGCTAGA CCATGGGTGC
-3 V W L L L T D T E M
1001 TTCTAGAGAT CTGACGGTTC ACTAAACGAG CTCTGCTTAT ATAGACCTCC
    AAGATCTCTA GACTGCCAAG TGATTTGCTC GAGACGAATA TATCTGGAGG
1051 CACCGTACAC GCCTACCGCC CATTGCGTC AACGGGGCGG GGTTATTACG
    GTGGCATGTG CGGATGGCGG GTAAACGCAG TTGCCCCGCC CCAATAATGC
1101 ACATTTTGGG AAGTCCCGTT GATTTTGGTG CAAAACAAA CTCCCATTGA
    TGTAAAACCT TTCAGGGCAA CTAAAACCAC GGTTTTGTTT GAGGGTAACT
1151 CGTCAATGGG GTGGAGACTT GGAAATCCCC GTGAGTCAAA CCGCTATCCA
    GCAGTTACCC CACCTCTGAA CCTTTAGGGG CACTCAGTTT GGCGATAGGT
1201 CGCCCATTGG TGTACTGCCA AAACCGCATC ACCATGGTAA TAGCGATGAC
    GCGGGTAACC ACATGACGGT TTTGGCGTAG TGGTACCATT ATCGCTACTG
1251 TAATACGTAG ATGTACTGCC AAGTAGGAAA GTCCCGTAAG GTCATGTACT
    ATTATGCATC TACATGACGG TTCATCCTTT CAGGGCATT CAGTACATGA
1301 GGGCATAATG CCAGGCGGGC CATTTACCGT CATTGACGTC AATAGGGGGC
    CCCGTATTAC GGTCCGCCCC GTAAATGGCA GTAACGTCAG TTATCCCCCG
1351 GGAATTGGCA TATGATACAC TTGATGTACT GCCAAGTGGG CAGTTTACCG
    CCTGAACCGT ATACTATGTG AACTACATGA CGGTTACCCC GTCAAATGGC
1401 TAAATACTCC ACCCATTGAC GTCAATGGAA AGTCCCTATT GGCGTTACTA
    ATTTATGAGG TGGGTAACCT CAGTTACCTT TCAGGGATAA CCGCAATGAT
1451 TGGGAACATA CGTCATTATT GACGTCAATG GGCGGGGGTC GTTGGGCGGT
    ACCCTTGATAT GCAGTAATAA CTGCAGTTAC CCGCCCCCAG CAACCCGCCA
1501 CAGCCAGGCG GGCCATTTAC CGTAAGTTAT GTAACGCGGA ACTCCATATA
    GTCGGTCCGC CCGGTAAATG GCATTCAATA CATTGCGCCT TGAGGTATAT
1551 TGGGCTATGA ACTAATGACC CCGTAATTGA TTAATATTAA TAACTAGTCA
    ACCCGATACT TGATTACTGG GGCATTAAT AATGATAATT ATTGATCAGT
1601 ATAATCAATG TCAACATGGC GGTCATATTG GACATGAGCC AATATAAATG
    TATTAGTTAC AGTTGTACCG CCAGTATAAC CTGTACTCGG TTATATTTAC
1651 TACATATTAT GATATAGATA CAACGTATGC AATGGCCAAT AGCCAATATT
    ATGTATAATA CTATATCTAT GTTGATACG TTACCGGTTA TCGGTTATAA
1701 GATTTATGCT ATATAACCAA TGACTAATAT GGCTAATTGC CAATATTGAT
    CTAAATACGA TATATTGGTT ACTGATTATA CCGATTAACG GTTATAACTA

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FIGURE 11-2

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1751 TCAATGTATA GATCTTCCAT ACCTACCAGT TCTGCGCCTG CAGCAATGCA
    AGTTACATAT CTAGAAGGTA TGGATGGTCA AGACGCGGAC GTCGTTACGT
1801 ACAACGTTGC CCGGATCTGC GATGATAAGC TGTCAAACAT GAGAATTGGT
    TGTTGCAACG GGCCTAGACG CTACTATTTCG ACAGTTTGTGTA CTCTTAACCA
1851 CGACTAGCTT GGCACGCCAG AAATCCGCGC GGTGGTTTTT GGGGGTCGGG
    GCTGATCGAA CCGTGCGGTC TTAGGCGCGC CCACCAAAAA CCCCCAGCCC
1901 GGTGTTTTGGC AGCCACAGAC GCCCAGGTGTT CGTGTGCGCG CAGTACATGC
    CCACAAACCG TCGGTGTCTG CGGGCCACAA GCACAGCGCG GTCATGTACG
1951 GGTCCATGCC CAGGCCATCC AAAAACCATG GGTCTGTCTG CTCAGTCCAG
    CCAGGTACGG GTCCGGTAGG TTTTGGGTAC CCAGACAGAC GAGTCAGGTC
2001 TCGTGGACCA GACCCACGC AACGCCCAA ATAATAACCC CCACGAACCA
    AGCACCTGGT CTGGGGTGCG TTGCGGGTTT TATTATTGGG GGTGCTTGGT
2051 TAAACCATT CCCCATGGGG ACCCCGTCCC TAACCCACGG GGCCAGTGGC
    ATTTGGTAAG GGGTACCCCC TGGGGCAGGG ATTGGGTGCC CCGGTCACCG
2101 TATGGCAGGG CCTGCCGCCC CGACGTTGGC TGCGAGCCCT GGGCCTTCAC
    ATACCGTCCC GGACGGCGGG GCTGCAACCG ACGCTCGGGA CCCGGAAGTG
2151 CCGAACTTGG GGGGTGGGGT GGGGAAAAGG AAGAAACGCG GGCGTATTGG
    GGCTTGAACC CCCCACCCCA CCCCTTTTCC TTCTTTGCGC CCGCATAACC
2201 CCCCATGGG GTCTCGGTGG GGTATCGACA GAGTGCCAGC CCTGGGACCG
    GGGGTTACCC CAGAGCCACC CCATAGCTGT CTCACGGTCG GGACCCTGGC
2251 AACCCCGCGT TTATGAACAA ACGACCCAAC ACCCGTGCGT TTTATTCTGT
    TTGGGGCGCA AATACTTGTT TGCTGGGTTG TGGGCACGCA AAATAAGACA
2301 CTTTTTATTG CCGTCATAGC GCGGGTTCCT TCCGGTATTG TCTCCTTCCG
    GAAAAATAAC GGCAGTATCG CGCCCAAGGA AGGCCATAAC AGAGGAAGGC
2351 TGTTTTCAGT AGCCTCCCCC ATCTCCCCTA TTCCTTTGCC CTCGGACGAG
    ACAAAGTCAA TCGGAGGGGG TAGAGGGGAT AAGGAAACGG GAGCCTGCTC
2401 TGCTGGGGCG TCGGTTTCCA CTATCGGCGA GTACTTCTAC ACAGCCATCG
    ACGACCCCGC AGCCAAAAGT GATAGCCGCT CATGAAGATG TGTCGGTAGC
2451 GTCCAGACGG CCGCGCTTCT GCGGGCGATT TGTGTACGCC CGACAGTCCC
    CAGGTCTGCC GGC CGAAGA CGCCCGCTAA ACACATGCGG GCTGTCAGGG
2501 GGCTCCGGAT CGGACGATTG CGTCGCATCG ACCCTGCGCC CAAGCTGCAT
    CCGAGGCC TA GCCTGCTAAC GCAGCGTAGC TGGGACGCGG GTTCGACGTA
2551 CATCGAAATT GCCGTCAACC AAGCTCTGAT AGAGTTGGTC AAGACCAATG
    GTAGCTTTAA CGGCAGTTGG TTCGAGACTA TCTCAACCAG TTCTGGTTAC
2601 CGGAGCATAT ACGCCCGGAG CCGCGGCGAT CCTGCAAGCT CCGGATGCCT
    GCCTCGTATA TGCGGGCCTC GGCGCCGCTA GGACGTTCTGA GGCTACGGA
2651 CCGCTCGAAG TAGCGCGTCT GCTGCTCCAT ACAAGCCAAC CACGGCCTCC
    GGCGAGCTTC ATCGCGCAGA CGACGAGGTA TGTTGCGTTG GTGCCGAGG
2701 AGAAGAAGAT GTTGCGGACC TCGTATTGGG AATCCCCGAA CATCGCCTCG
    TCTTCTTCTA CAACCGCTGG AGCATAACCC TTAGGGGCTT GTAGCGGAGC
2751 CTCCAGTCAA TGACCGCTGT TATGCGGCCA TTGTCCGTCA GGACATTGTT
    GAGGTCAGTT ACTGGCGACA ATACGCCGGT AACAGGCAGT CCTGTAACAA
2801 GGAGCCGAAA TCCGCGTGCA CGAGGTGCCG GACTTCGGGG CAGTCCTCGG
    CCTCGGCTTT AGGCGCACGT GCTCCACGGC CTGAAGCCCC GTCAGGAGCC
2851 CCCAAAGCAT CAGCTCATCG AGAGCCTGCG CGACGGACGC ACTGACGGTG
    GGGTTTCGTA GTCGAGTAGC TCTCGGACGC GCTGCCTGCG TGACTGCCAC

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FIGURE 11-3

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2901  TCGTCCATCA CAGTTTGCCA GTGATACACA TGGGGATCAG CAATCGCGCA
      AGCAGGTAAGT GTCAAACGGT CACTATGTGT ACCCCTAGTC GTTAGCGCGT
2951  TATGAAATCA CGCCATGTAG TGTATTGACC GATTCCCTGC GGTCCGAATG
      ATACTTTAGT GCGGTACATC ACATAACTGG CTAAGGAACG CCAGGCTTAC
3001  GGCCGAACCC GCTCGTCTGG CTAAGATCGG CCGCAGCGAT CGCATCCATG
      CCGGCTTGGG CGAGCAGACC GATTCTAGCC GGCCTCGCTA GCGTAGGTAC
3051  GCCTCCGCGA CCGGCTGCAG AACAGCGGGC AGTTCGGTTT CAGGCAGGTC
      CGGAGGCGCT GGCCGACGTC TTGTCGCCCC TCAAGCCAAA GTCCGTCCAG
3101  TTGCAACGTG ACACCCCTGTG CACGGCGGGA GATGCAATAG GTCAGGCTCT
      AACGTTGCAC TGTGGGACAC GTGCCGCCCT CTACGTTATC CAGTCCGAGA
3151  CGCTGAATTC CCCAATGTCA AGCACTTCCG GAATCGGGAG CGCGGCCGAT
      GCGACTTAAG GGGTTACAGT TCGTGAAGGC CTTAGCCCTC GCGCCGGCTA
3201  GCAAAGTGCC GATAAACATA ACGATCTTTG TAGAAACCAT CGGCGCAGCT
      CGTTTCACGG CTATTTGTAT TGCTAGAAAC ATCTTTGGTA GCCGCGTCGA
3251  ATTTACCCGC AGGACATATC CACGCCCTCC TACATCGAAG CTGAAAGCAC
      TAAATGGGCG TCCTGTATAG GTGCGGGAGG ATGTAGCTTC GACTTTCGTG
3301  GAGATTCTTC GCCCTCCGAG AGCTGCATCA GGTGCGAGAC GCTGTCGAAC
      CTCTAAGAAG CGGGAGGCTC TCGACGTAGT CCAGCCTCTG CGACAGCTTG
3351  TTTTCGATCA GAAACTTCTC GACAGACGTC GCGGTGAGTT CAGGCTTTTTT
      AAAAGCTAGT CTTTGAAGAG CTGTCTGCAG CGCCACTCAA GTCCGAAAAA
3401  CATATCTCAT TGCCCGGGAT CTGCGGCACG CTGTTGACGC TGTTAAGCGG
      GTATAGAGTA ACGGGCCCTA GACGCCGTGC GACAACTGCG ACAATTCGCC
3451  GTCGCTGCAG GGTGCTCGG TGTTGAGGC CACACGCGTC ACCTTAATAT
      CAGCGACGTC CCAGCGAGCC ACAAGCTCCG GTGTGCGCAG TGGAATTATA
3501  GCGAAGTGGA CCTGGGACCG CGCCGCCCCG ACTGCATCTG CGTGTTTCGAA
      CGCTTCACCT GGACCCTGGC GCGGCGGGGC TGACGTAGAC GCACAAGCTT
3551  TTCGCCAATG ACAAGACGCT GGGCGGGGTT TGTGTCATCA TAGAACTAAA
      AAGCGGTTAC TGTTCTGCGA CCCGCCCAA ACACAGTAGT ATCTTGATTT
3601  GACATGCAAA TATATTTCTT CCGGGGACAC CGCCAGCAAA CGCGAGCAAC
      CTGTACGTTT ATATAAAGAA GGCCCCGTGT GCGGTGCTTT GCGCTCGTTG
3651  GGGCCACGGG GATGAAGCAG GGCATGGCGG CCGACGCGCT GGGCTACGTC
      CCCGGTGCCC CTACTTCGTC CCGTACCGCC GGCTGCGCGA CCCGATGCAG
3701  TTGCTGGCGT TCGCGACGCG AGGCTGGATG GCCTTCCCCA TTATGATTCT
      AACGACCGCA AGCGCTGCGC TCCGACCTAC CGGAAGGGGT AATACTAAGA
3751  TCTCGCTTCC GGCGGCATCG GGATGCCCCG GTTGCGAGGC ATGCTGTCCA
      AGAGCGAAGG CCGCCGTAGC CCTACGGGCG CAACGTCCGG TACGACAGGT
3801  GGCAGGTAAG TGACGACCAT CAGGGACAGC TTCAAGGATC GCTCGCGGCT
      CCGTCCATCT ACTGCTGGTA GTCCCTGTGCG AAGTTCCTAG CGAGCGCCGA
3851  CTTACCAGCC TAACCTTCGAT CACTGGACCG CTGATCGTCA CGGCGATTTA
      GAATGGTCGG ATTGAAGCTA GTGACCTGGC GACTAGCAGT GCCGCTAAAT
3901  TGCCGCCTCG GCGAGCACAT GGAACGGGTT GGCATGGATT GTAGGCGCCG
      ACGGCGGAGC CGCTCGTGTA CCTTGCCCAA CCGTACCTAA CATCCGCGGC
3951  CCCTATACCT TGTCTGCCTC CCCGCGTTGC GTCGCGGTGC ATGGAGCCGG
      GGGATATGGA ACAGACGGAG GGGCGCAACG CAGCGCCACG TACCTCGGCC
4001  GCCACCTCGA CCTGAATGGA AGCCGGCGGC ACCTCGCTAA CGGATTACAC
      CGGTGGAGCT GGAATTACCT TCGGCCGCCG TGGAGCGATT GCCTAAGTGG

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FIGURE 11-4

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4051 ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAACTG TGAATGCGCA
    TGAGGTTCCT AACCTCGGTT AGTTAAGAAC GCCTCTTGAC ACTTACGCGT
4101 AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC
    TTGGTTGGGA ACCGTCTTGT ATAGGTAGCG CAGGCGGTAG AGGTCGTCGG
4151 GCACGCGGCG CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG
    CGTGCGCCGC GTCGTTTTCC GGTCCCTGGC ATTTTCCGG CGCAACGACC
4201 CGTTTTTCCA TAGGCTCCGC CCCCTGACG AGCATCACAA AAATCGACGC
    GCAAAAAGGT ATCCGAGGCG GGGGGACTGC TCGTAGTGTT TTTAGCTGCG
4251 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT
    AGTTCAGTCT CCACCGCTTT GGGCTGTCTT GATATTTCTA TGGTCCGCAA
4301 TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCGACC CTGCCGCTTA
    AGGGGGACCT TCGAGGGAGC ACGCGAGAGG ACAAGGCTGG GACGGCGAAT
4351 CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT
    GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGCACCG CGAAAGAGTA
4401 AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTT GCTCCAAGCT
    TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA
4451 GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC GCCTTATCCG
    CCCGACACAC GTGCTTGGGG GGCAAGTCGG GCTGGCGACG CGGAATAGGC
4501 GTAAGTATCG TCTTGAGTCC AACC CGGTAA GACACGACTT ATCGCCACTG
    CATTGATAGC AGAACTCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC
4551 GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC
    CGTCGTGCGT GACCATGTCT CTAATCGTCT CGCTCCATAC ATCCGCCACG
4601 TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG
    ATGTCTCAAG AACTTCACCA CCGGATTGAT GCCGATGTGA TCTTCCTGTC
4651 TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT
    ATAAACCATA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTCTCAA
4701 GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTTT
    CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA
4751 TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC
    ACAAACGTTT GTCGTCTAAT GCGCGTCTTT TTTTCTTAGA GTTCTTCTAG
4801 CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAATCACGT
    GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA
4851 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT
    ATTCCCTAAA ACCAGTACTC TAATAGTTTT TCCTAGAAGT GGATCTAGGA
4901 TTTAAATTAA AAATGAAGTT TTAATCAAT CTAAAGTATA TATGAGTAAA
    AAATTTAATT TTTACTTCAA AATTTAGTTA GATTTTCATAT ATACTCATTT
4951 CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG
    GAACCAGACT GTCAATGGTT ACGAATTAGT CACTCCGTGG ATAGAGTCGC
5001 ATCTGTCTAT TTCGTTTCATC CATAGTTGCC TGAATCCCCG TCGTGTAGAT
    TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGGC AGCACATCTA
5051 AACTACGATA CGGGAGGGCT TACCATCTGG CCCAGTGCT GCAATGATAC
    TTGATGCTAT GCCCTCCCGA ATGGTAGACC GGGGTCACGA CGTTACTATG
5101 CGCGAGACCC ACGCTCACC GCTCCAGATT TATCAGCAAT AAACCAGCCA
    GCGCTCTGGG TGCGAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCGGT
5151 GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGCTCCAT
    CGGCCTTCCC GGCTCGCGTC TTCACCAGGA CGTTGAAATA GGCGGAGGTA

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FIGURE 11-5


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5201 CCAGTCTATT AATTGTTGCC GGGAAAGCTAG AGTAAGTAGT TCGCCAGTTA
      GGTCAGATAA TTAACAACGG CCCTTCGATC TCATTCATCA AGCGGTCAAT
5251 ATAGTTTTCG CAACGTTGTT GCCATTGCTG CAGGCATCGT GGTGTCACGC
      TATCAAACGC GTTGCAACAA CGGTAACGAC GTCCGTAGCA CCACAGTGCG
5301 TCGTCGTTTG GTATGGCTTC ATTCTAGCTCC GGTTCCTAAC GATCAAGGCG
      AGCAGCAAAC CATACCGAAG TAAGTCGAGG CCAAGGGTTG CTAGTTCCGC
5351 AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC
      TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCAATCG AGGAAGCCAG
5401 CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT
      GAGGCTAGCA ACAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA
5451 ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT
      TACCGTCGTG ACGTATTAAG AGAATGACAG TACGGTAGGC ATTCTACGAA
5501 TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC
      AAGACACTGA CCACTCATGA GTTGGTTCAG TAAGACTCTT ATCACATACG
5551 GGCGACCGAG TTGCTCTTGC CCGGCGTCAA CACGGGATAA TACCGCGCCA
      CCGCTGGCTC AACGAGAACG GGCCGCAGTT GTGCCCTATT ATGGCGCGGT
5601 CATAGCAGAA CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG
      GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAG GAAGCCCCGC
5651 AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCG ATGTAACCCA
      TTTTGAGAGT TCCTAGAATG GCGACAACCTC TAGGTCAAGC TACATTGGGT
5701 CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT
      GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAGTG GTCGCAAAGA
5751 GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGGC
      CCCACTCGTT TTTGTCCTTC CGTTTTACGG CGTTTTTTCC CTTATTCCCCG
5801 GACACGGAAG TGTTGAATAC TCATACTCTT CCTTTTTCAG TATTATTGAA
      CTGTGCCTTT ACAACTTATG AGTATGAGAA GGAAAAAGTT ATAATAACTT
5851 GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT
      CGTAAATAGT CCCAATAACA GAGTACTCGC CTATGTATAA ACTTACATAA
5901 TAGAAAAATA AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC
      ATCTTTTAT TTTGTTTATC CCAAGGCGCG TGTAAGGGG CTTTTCACGG
5951 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAAATA
      TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATTGG ATATTTTAT
6001 GGCGTATCAC GAGGCCCTTT CGTCTTCAAG AATTCTCATG TTTGACAGCT
      CCGCATAGTG CTCCGGGAAA GCAGAAGTTC TTAAGAGTAC AACTGTCTGA
6051 TATCATCGAT AAGCTGATCC TCACAGGCCG CACCCAGCTT TTCTTCCGTT
      ATAGTAGCTA TTCGACTAGG AGTGTCCGGC GTGGGTCGAA AAGAAGGCAA
6101 GCCCCAGTAG CATCTCTGTC TGGTGACCTT GAAGAGGAAG AGGAGGGGTC
      CGGGGTCATC GTAGAGACAG ACCACTGGAA CTTCTCCTTC TCCTCCCCAG
6151 CCGAGAATCC CCATCCCTAC CGTCCAGCAA AAAGGGGGAC GAGGAATTTG
      GGCTCTTAGG GGTAGGGATG GCAGGTCGTT TTTCCCCCTG CTCCTTAAAC
6201 AGGCCTGGCT TGAGGCTCAG GACGCAAATC TTGAGGATGT TCAGCGGGAG
      TCCGGACCGA ACTCCGAGTC CTGCGTTTAG AACTCCTACA AGTCGCCCTC
6251 TTTTCCGGGC TGCGAGTAAT TGGTGATGAG GACGAGGATG GTTCGGAGGA
      AAAAGGCCCG ACGCTCATTA ACCACTACTC CTGCTCCTAC CAAGCCTCCT
6301 TGGGGAATTT TCAGACCTGG ATCTGTCTGA CAGCGACCAT GAAGGGGATG
      ACCCCTTAAA AGTCTGGACC TAGACAGACT GTCGCTGGTA CTTCCCCTAC

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FIGURE 11-6

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6351  AGGGTGGGGG GGCTGTTGGA GGGGGCAGGA GTCTGCACTC CCTGTATTCA
      TCCCACCCCC CCGACAACCT CCCCCGTCCT CAGACGTGAG GGACATAAGT
6401  CTGAGCGTCG TCTAATAAAG ATGTCTATTG ATCTCTTTTA GTGTGAATCA
      GACTCGCAGC AGATTATTTT TACAGATAAC TAGAGAAAAT CACACTTAGT
6451  TGTCTGACGA GGGGCCAGGT ACAGGACCTG GAAATGGCCT AGGAGAGAAG
      ACAGACTGCT CCCCAGTCCA TGTCTGGAC CTTTACCGGA TCCTCTCTTC
6501  GGAGACACAT CTGGACCAGA AGGCTCCGGC GGCAGTGGAC CTCAAAGAAG
      CCTCTGTGTA GACCTGGTCT TCCGAGGCCG CCGTCACCTG GAGTTTCTTC
6551  AGGGGGTGAT AACCATGGAC GAGGACGGGG AAGAGGACGA GGACGAGGAG
      TCCCCACTA TTGGTACCTG CTCCTGCCCC TTCTCCTGCT CCTGCTCCTC
6601  GCGGAAGACC AGGAGCCCCG GCGGCTCAG GATCAGGGCC AAGACATAGA
      CGCTTCTGCG TCCTCGGGGC CCGCCGAGTC CTAGTCCCGG TTCTGTATCT
6651  GATGGTGTCC GGAGACCCCA AAAACGTCCA AGTTGCATTG GCTGCAAAGG
      CTACCACAGG CCTCTGGGGT TTTTGCAGGT TCAACGTAAC CGACGTTTCC
6701  GACCCACGGT GGAACAGGAG CAGGAGCAGG AGCGGGAGGG GCAGGAGCAG
      CTGGGTGCCA CCTTGTCTC GTCCTCGTCC TCGCCCTCCC CGTCCCTCGTC
6751  GAGGGGCAGG AGCAGGAGGA GGGGCAGGAG CAGGAGGAGG GGCAGGAGGG
      CTCCCCGTCC TCGTCTCCT CCCCCTCCTC GTCTCTCTCC CCGTCTCTCC
6801  GCAGGAGGGG CAGGAGGGGC AGGAGCAGGA GGAGGGGCAG GAGCAGGAGG
      CGTCTCTCCC GTCTCTCCCG TCCTCGTCTC CCTCCCCGTC CTCGTCTCTC
6851  AGGGGCAGGA GGGGCAGGAG GGCAGGAGC AGGAGGAGGG GCAGGAGCAG
      TCCCCGTCT CCCCCTCTC CCGTCTCTC TCCTCTCTCC CGTCTCTCTC
6901  GAGGAGGGGC AGGAGGGGCA GGAGCAGGAG GAGGGGCAGG AGGGGCAGGA
      CTCTCTCCCC TCCTCCCCGT CCTCGTCTC CTCCCCGTCC TCCCCGTCTC
6951  GGGGCAGGAG CAGGAGGAGG GGCAGGAGCA GGAGGAGGGG CAGGAGGGGC
      CCCCCTCTC GTCTCTCTC CCGTCTCTC CCTCTCTCCC GTCTCTCCCC
7001  AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG AGGGGCAGGA GCAGGAGGAG
      TCCTCGTCTC CTCTCCCCG TCCTCCCCG TCCTCCCCG TCCTCCCCG
7051  GGGCAGGAGC AGGAGGGGCA GGAGGGGCAG GAGGGGCAGG AGCAGGAGGG
      CCGTCTCTC TCCTCCCCG CTCTCCCCG CTCTCCCCG TCCTCTCTCC
7101  GCAGGAGCAG GAGGAGGGGC AGGAGGGGCA GGAGGGGCAG GAGCAGGAGG
      CGTCTCTCTC CTCTCCCCG TCCTCCCCG CTCTCCCCG CTCGTCTCTC
7151  GGCAGGAGCA GGAGGGGCAG GAGCAGGAGG GGCAGGAGCA GGAGGGGCAG
      CCGTCTCTC CTCTCCCCG CTCGTCTCTC CCGTCTCTC CCTCTCTCTC
7201  GAGGGGCAGG AGCAGGAGGG GCAGGAGGGG CAGGAGCAGG AGGGGCAGGA
      CTCCCCGTCC TCGTCTCTC CGTCTCTCTC GTCTCTCTC TCCCCGTCTC
7251  GGGGCAGGAG CAGGAGGAGG GGCAGGAGGG GCAGGAGCAG GAGGAGGGGC
      CCCCCTCTC GTCTCTCTC CCGTCTCTC CGTCTCTCTC CTCTCTCTCC
7301  AGGAGGGGCA GGAGCAGGAG GGCAGGAGG GGCAGGAGCA GGAGGGGCAG
      TCCTCCCCG CTCTCTCTC CCGTCTCTC CCGTCTCTC CCTCTCTCTC
7351  GAGGGGCAGG AGCAGGAGGG GCAGGAGGGG CAGGAGCAGG AGGAGGGGCA
      CTCCCCGTCC TCGTCTCTC CGTCTCTCTC GTCTCTCTC TCCTCTCTCT
7401  GGAGCAGGAG GGGCAGGAGC AGGAGGTGGA GGCCGGGGTC GAGGAGGCAG
      CCTCGTCTC CCGTCTCTC TCCTCTCTC CCGGGGGGTC CTCCTCTCTC
7451  TGGAGGCCGG GGTCTGAGGAG GTAGTGGAGG CCGGGGGTCA GGAGGTAGTG
      ACCTCCGGCC CCAGCTCTC CATCACCTC GGGGGGAGCT CCTCTCTCTC

```

FIGURE 11-7

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7501 GAGGCCGCCG GGGTAGAGGA CGTGAAAGAG CCAGGGGGGG AAGTCGTGAA
      CTCCGGCGGC CCCATCTCCT GCACTTTCTC GGTCCCCCCC TTCAGCACTT
7551 AGAGCCAGGG GGAGAGGTCG TGGACGTGGA GAAAAGAGGC CCAGGAGTCC
      TCTCGGTCCC CCTCTCCAGC ACCTGCACCT CTTTTCCTCCG GGTCTCTCAGG
7601 CAGTAGTCAG TCATCATCAT CCGGGTCTCC ACCGCGCAGG CCCCTCCAG
      GTCATCAGTC AGTAGTAGTA GGCCAGAGG TGGCGCGTCC GGGGGAGGTC
7651 GTAGAAGGCC ATTTTTCAC CCTGTAGGGG AAGCCGATTA TTTTGAATAC
      CATCTTCCGG TAAAAAGGTG GGACATCCCC TTCGGCTAAT AAAACTTATG
7701 CACCAAGAAG GTGGCCAGA TGGTGAGCCT GACGTGCCCC CGGGAGCGAT
      GTGGTTCTTC CACCGGGTCT ACCACTCGGA CTGCACGGGG GCCCTCGCTA
7751 AGAGCAGGGC CCCGCAGATG ACCCAGGAGA AGGCCCAAGC ACTGGACCCC
      TCTCGTCCCG GGGCGTCTAC TGGGTCTCT TCCGGGTTCC TGACCTGGGG
7801 GGGGTCAGGG TGATGGAGGC AGGCGCAAAA AAGGAGGGTG GTTTGGAAAG
      CCCAGTCCC ACTACCTCCG TCCGCGTTTT TTCTCCAC CAAACCTTTC
7851 CATCGTGGTC AAGGAGGTTT CAACCCGAAA TTTGAGAACA TTGCAGAAGG
      GTAGCACCAG TTCCTCCAAG GTTGGGCTTT AAACCTTTGT AACGTCTTCC
7901 TTAAAGAGCT CTCCTGGCTA GGAGTCACGT AGAAAGGACT ACCGACGAAG
      AAATTCTCGA GAGGACCGAT CCTCAGTGCA TCTTTCCTGA TGGCTGCTTC
7951 GAACCTGGGT CGCCGGTGTG TTCGTATATG GAGGTAGTAA GACCTCCCTT
      CTTGAACCCA GCGGCCACAC AAGCATATAC CTCCATCATT CTGGAGGGAA
8001 TACAACCTAA GGCGAGGAAC TGCCCTTGCT ATTCCACAAT GTCGTCTTAC
      ATGTTGGATT CCGCTCCTTG ACGGGAACGA TAAGGTGTTA CAGCAGAATG
8051 ACCATTGAGT CGTCTCCCCT TTGGAATGGC CCCTGGACCC GGCCACAAC
      TGGTAACTCA GCAGAGGGGA AACCTTACCG GGGACCTGGG CCGGGTGTG
8101 CTGGCCCGCT AAGGGAGTCC ATTGCTGTGT ATTTTCATGGT CTTTTTACAA
      GACCGGGCGA TTCCCTCAGG TAACAGACAA TAAAGTACCA GAAAAATGTT
8151 ACTCATATAT TTGCTGAGGT TTTGAAGGAT GCGATTAAGG ACCTTGTTAT
      TGAGTATATA AACGACTCCA AAACCTTCTA CGCTAATTCC TGGAACAATA
8201 GACAAAGCCC GCTCCTACCT GCAATATCAG GGTGACTGTG TGCAGCTTTG
      CTGTTTCGGG CGAGGATGGA CGTTATAGTC CCACTGACAC ACGTCGAAAC
8251 ACGATGGAGT AGATTTGCCT CCCTGGTTTC CACCTATGGT GGAAGGGGCT
      TGCTACCTCA TCTAAACGGA GGGACCAAAG GTGGATACCA CCTTCCCCGA
8301 GCCGCGGAGG GTGATGACGG AGATGACGGA GATGAAGGAG GTGATGGAGA
      CGGCGCCTCC CACTACTGCC TCTACTGCCT CTACTTCCTC CACTACCTCT
8351 TGAGGGTGAG GAAGGGCAGG AGTGATGTAA CTTGTTAGGA GACGCCCTCA
      ACTCCCACTC CTTCCCGTCC TCACTACATT GAACAATCCT CTGCGGGAGT
8401 ATCGTATTAA AAGCCGTGTA TTCCCCGCA CTAAAGAATA AATCCCCAGT
      TAGCATAATT TTCGGCACAT AAGGGGGCGT GATTTCTTAT TTAGGGGTCA
8451 AGACATCATG CGTGCTGTTG GTGTATTTCT GGCCATCTGT CTTGTCACCA
      TCTGTAGTAC GCACGACAAC CACATAAAGA CCGGTAGACA GAACAGTGGT
8501 TTTTCGTCCCT CCAACATGG GGCAATTGGG CATACCCATG TTGTCACGTC
      AAAAGCAGGA GGGTTGTACC CCGTTAACCC GTATGGGTAC AACAGTGCAG
8551 ACTCAGCTCC GCGCTCAACA CCTTCTCGCG TTGGAAAACA TTAGCGACAT
      TGAGTCGAGG CGCGAGTTGT GGAAGAGCGC AACCTTTTGT AATCGCTGTA
8601 TTACCTGGTG AGCAATCAGA CATGCGACGG CTTTAGCCTG GCCTCCTTAA
      AATGGACCAC TCGTTAGTCT GTACGCTGCC GAAATCGGAC CGGAGGAATT

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FIGURE 11-8

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8651  ATTCACCTAA GAATGGGAGC AACCAGCATG CAGGAAAAGG ACAAGCAGCG
      TAAGTGGATT CTTACCCTCG TTGGTCGTAC GTCCTTTTCC TGTTTCGTCG
8701  AAAATTCACG CCCCCTTGGG AGGTGGCGGC ATATGCAAAG GATAGCACTC
      TTTTAAGTGC GGGGGAACCC TCCACCGCCG TATACGTTTC CTATCGTGAG
8751  CCACTCTACT ACTGGGTATC ATATGCTGAC TGTATATGCA TGAGGATAGC
      GGTGAGATGA TGACCCATAG TATACGACTG ACATATACGT ACTCCTATCG
8801  ATATGCTACC CGGATACAGA TTAGGATAGC ATATACTACC CAGATATAGA
      TATACGATGG GCCTATGTCT AATCCTATCG TATATGATGG GTCTATATCT
8851  TTAGGATAGC ATATGCTACC CAGATATAGA TTAGGATAGC CTATGCTACC
      AATCCTATCG TATACGATGG GTCTATATCT AATCCTATCG GATACGATGG
8901  CAGATATAAA TTAGGATAGC ATATACTACC CAGATATAGA TTAGGATAGC
      GTCTATATTT AATCCTATCG TATATGATGG GTCTATATCT AATCCTATCG
8951  ATATGCTACC CAGATATAGA TTAGGATAGC CTATGCTACC CAGATATAGA
      TATACGATGG GTCTATATCT AATCCTATCG GATACGATGG GTCTATATCT
9001  TTAGGATAGC ATATGCTACC CAGATATAGA TTAGGATAGC ATATGCTATC
      AATCCTATCG TATACGATGG GTCTATATCT AATCCTATCG TATACGATAG
9051  CAGATATTTG GGTAGTATAT GCTACCCAGA TATAAATTAG GATAGCATAT
      GTCTATAAAC CCATCATATA CGATGGGTCT ATATTTAATC CTATCGTATA
9101  ACTACCCCTAA TCTCTATTAG GATAGCATAT GCTACCCGGA TACAGATTAG
      TGATGGGATT AGAGATAATC CTATCGTATA CGATGGGCCT ATGTCTAATC
9151  GATAGCATAT ACTACCCAGA TATAGATTAG GATAGCATAT GCTACCCAGA
      CTATCGTATA TGATGGGTCT ATATCTAATC CTATCGTATA CGATGGGTCT
9201  TATAGATTAG GATAGCCTAT GCTACCCAGA TATAAATTAG GATAGCATAT
      ATATCTAATC CTATCGGATA CGATGGGTCT ATATTTAATC CTATCGTATA
9251  ACTACCCAGA TATAGATTAG GATAGCATAT GCTACCCAGA TATAGATTAG
      TGATGGGTCT ATATCTAATC CTATCGTATA CGATGGGTCT ATATCTAATC
9301  GATAGCCTAT GCTACCCAGA TATAGATTAG GATAGCATAT GCTATCCAGA
      CTATCGGATA CGATGGGTCT ATATCTAATC CTATCGTATA CGATAGGTCT
9351  TATTTGGGTA GTATATGCTA CCCATGGCAA CATTAGCCCA CCGTGCTCTC
      ATAAACCCAT CATATACGAT GGGTACCGTT GTAATCGGGT GGCACGAGAG
9401  AGCGACCTCG TGAATATGAG GACCAACAAC CCTGTGCTTG GCGCTCAGGC
      TCGCTGGAGC ACTTATACTC CTGGTTGTTG GGACACGAAC CGCGAGTCCG
9451  GCAAGTGTGT GTAATTTGTC CTCCAGATCG CAGCAATCGC GCCCCCTATCT
      CGTTCACACA CATTAACAG GAGGTCTAGC GTCGTTAGCG CGGGGATAGA
9501  TGGCCCGCCC ACCTACTTAT GCAGGTATTC CCCGGGGTGC CATTAGTGGT
      ACCGGGCGGG TGGATGAATA CGTCCATAAG GGGCCCCACG GTAATCACCA
9551  TTTGTGGGCA AGTGGTTTGA CCGCAGTGGT TAGCGGGGTT ACAATCAGCC
      AAACACCCGT TCACCAAAC TGGCGTCACCA ATCGCCCCAA TGTTAGTCGG
9601  AAGTTATTAC ACCCTTATTT TACAGTCCAA AACC GCAGGG CGGCGTGTGG
      TTCAATAATG TGGGAATAAA ATGTCAGGTT TTGGCGTCCC GCCGCACACC
9651  GGGCTGACGC GTGCCCCCAC TCCACAATTT CAAAAAAAAG AGTGCCACT
      CCCGACTGCG CACGGGGGTG AGGTGTTAAA GTTTTTTTTC TCACCGGTGA
9701  TGTCTTTGTT TATGGGCCCC ATTGGCGTGG AGCCCCGTTT AATTTTCGGG
      ACAGAAACAA ATACCCGGGG TAACCGCACC TCGGGGCAAA TAAAAAGCCC
9751  GGTGTTAGAG ACAACAGTG GAGTCCGCTG CTGTCGGCGT CCACTCTCTT
      CCACAATCTC TGTTGGTCAC CTCAGGCGAC GACAGCCGCA GGTGAGAGAA

```

FIGURE 11-9

9801	TCCCCTTGTT	ACAAATAGAG	TGTAACAACA	TGGTTCACCT	GTCTTGGTCC
	AGGGGAACAA	TGTTTATCTC	ACATTGTTGT	ACCAAGTGGA	CAGAACCCAGG
9851	CTGCCTGGGA	CACATCTTAA	TAACCCCAGT	ATCATATTGC	ACTAGGATTA
	GACGGACCCCT	GTGTAGAATT	ATTGGGGTCA	TAGTATAACG	TGATCCCTAAT
9901	TGTGTTGCCC	ATAGCCATAA	ATTCGTGTGA	GATGGACATC	CAGTCTTTAC
	ACACAACGGG	TATCGGTATT	TAAGCACACT	CTACCTGTAG	GTCAGAAATG
9951	GGCTTGTCCT	CACCCCATGG	ATTTCTATTG	TTAAAGATAT	TCAGAAATGTT
	CCGAACAGGG	GTGGGGTACC	TAAAGATAAC	AATTTCTATA	AGTCTTACAA
10001	TCATTCCCTAC	ACTAGTATTT	ATTGCCCAAG	GGGTTTGTGA	GGGTTATATT
	AGTAAGGATG	TGATCATAAA	TAACGGGTTC	CCCAAACACT	CCCAATATAA
10051	GGTGTCCATAG	CACAATGCCA	CCACTGAACC	CCCCGTCCAA	ATTTTATTCT
	CCACAGTATC	GTGTTACGGT	GGTGACTTGG	GGGGCAGGTT	TAAAATAAGA
10101	GGGGGCGTCA	CCTGAAACCT	TGTTTTTCGAG	CACCTCACAT	ACACCTTACT
	CCCCCGCAGT	GGACTTTGGA	ACAAAAGCTC	GTGGAGTGTA	TGTGGAATGA
10151	GTTCCACAAC	CAGCAGTTAT	TCTATTAGCT	AAACGAAGGA	GAATGAAGAA
	CAAGTGTTGA	GTCGTCAATA	AGATAATCGA	TTTGCTTCCT	CTTACTTCTT
10201	GCAGGCGAAG	ATTCAGGAGA	GTTCACTGCC	CGCTCCTTGA	TCTTCAGCCA
	CGTCCGCTTC	TAAGTCCTCT	CAAGTGACGG	GCGAGGAAC	AGAAGTCGGT
10251	CTGCCCTTGT	GACTAAAATG	GTTCACTACC	CTCGTGGAAT	CCTGACCCCA
	GACGGGAACA	CTGATTTTAC	CAAGTGATGG	GAGCACCTTA	GGACTGGGGT
10301	TGTAAATAAA	ACCGTGACAG	CTCATGGGGT	GGGAGATATC	GCTGTTCCCT
	ACATTTATTT	TGGCACTGTC	GAGTACCCCA	CCCTCTATAG	CGACAAGGAA
10351	AGGACCCTTT	TACTAACCTT	AATTTCGATAG	CATATGCTTC	CCGTTGGGTA
	TCCTGGGAAA	ATGATTGGGA	TTAAGCTATC	GTATACGAAG	GGCAACCCAT
10401	ACATATGCTA	TTGAATTAGG	GTTAGTCTGG	ATAGTATATA	CTACTACCCG
	TGTATACGAT	AAC'TTAATCC	CAATCAGACC	TATCATATAT	GATGATGGGC
10451	GGAAGCATAT	GCTACCCGTT	TAGGGTTAAC	AAGGGGGCCT	TATAAACACT
	CCTTCGTATA	CGATGGGCAA	ATCCCAATTG	TTCCCCCGGA	ATATTTGTGA
10501	ATTGCTAATG	CCCTCTTGAG	GGTCCGCTTA	TCGGTAGCTA	CACAGGCCCC
	TAACGATTAC	GGGAGAACTC	CCAGGCGAAT	AGCCATCGAT	GTGTCCGGGG
10551	TCTGATTGAC	GTTGGTGTAG	CCTCCCGTAG	TCTTCCTGGG	CCCCTGGGAG
	AGACTAACTG	CAACCACATC	GGAGGGCATC	AGAAGGACCC	GGGGACCCTC
10601	GTACATGTCC	CCCAGCATTG	GTGTAAGAGC	TTCAGCCAAG	AGTTACACAT
	CATGTACAGG	GGGTCGTAAC	CACATTCTCG	AAGTCGGTTC	TCAATGTGTA
10651	AAAGGCAATG	TTGTGTTGCA	GTCCACAGAC	TGCAAAGTCT	GCTCCAGGAT
	TTTCCGTTAC	AACACAACGT	CAGGTGTCTG	ACGTTTCAGA	CGAGGTCCTA
10701	GAAAGCCACT	CAGTGTGGC	AAATGTGCAC	ATCCATTTAT	AAGGATGTCA
	CTTTCGGTGA	GTCACAACCG	TTTACACGTG	TAGGTAAATA	TTCCTACAGT
10751	ACTACAGTCA	GAGAACCCCT	TTGTGTTTGG	TCCCCCCCCG	TGTCACATGT
	TGATGTCAGT	CTCTTGGGGA	AACACAAACC	AGGGGGGGGC	ACAGTGTACA
10801	GGAACAGGGC	CCAGTTGGCA	AGTTGTACCA	ACCAACTGAA	GGGATTACAT
	CCTTGTTCCCG	GGTCAACCGT	TCAACATGGT	TGGTTGACTT	CCCTAATGTA
10851	GCACTGCCCC	GCGAAGAAGG	GGCAGAGATG	CCGTAGTCAG	GTTTAGTTTCG
	CGTGACGGGG	CGCTTCTTCC	CCGTCTCTAC	GGCATCAGTC	CAAATCAAGC
10901	TCCGGCGGCG	GGGCTCTAGA	GTCGACCGGT	CATGGCTGCG	CCCCGACACC
	AGGCCGCCGC	CCCGAGATCT	CAGCTGGCCA	GTACCGACGC	GGGGCTGTGG

FIGURE 11-10

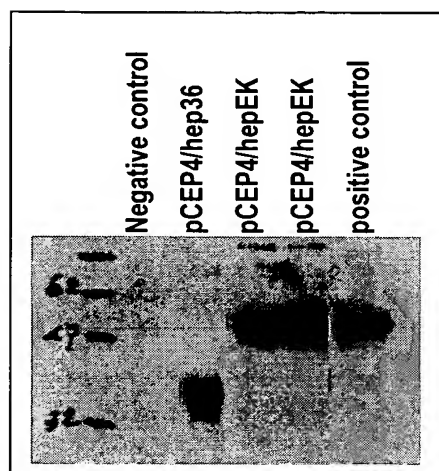
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10951 CGCCAACACC CGCTGACGCG CCCTGACGGG CTTGTCTGCT CCCGGCATCC
      GCGGTTGTGG GCGACTGCGC GGGACTGCCC GAACAGACGA GGGCCGTAGG
11001 GCTTACAGAC AAGCTGTGAC CGTCTCCGGG AGCTGCATGT GTCAGAGGTT
      CGAATGTCTG TTCGACACTG GCAGAGGCCC TCGACGTACA CAGTCTCCAA
11051 TTCACCGTCA TCACCGAAAC GCGCGAGGCA GCCGGATCAT AATCAGCCAT
      AAGTGGCAGT AGTGGCTTTG CGCGCTCCGT CGGCCTAGTA TTAGTCGGTA
11101 ACCACATTTG TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CCACCTCCCC
      TGGTGTAAC ATCTCCAAAA TGAACGAAAT TTTTGGAGG GGTGGAGGGG
11151 CTGAACCTGA AACATAAAAT GAATGCAATT GTTGTTGTTA ACTTGTTTAT
      GACTTGGACT TTGTATTTTA CTTACGTAA CAACAACAAT TGAACAAATA
11201 TGCAGCTTAT AATGGTTACA AATAAAGCAA TAGCATCACA AATTTACAAA
      ACGTCGAATA TTACCAATGT TTATTTTCGT ATCGTAGTGT TTAAAGTGTT
11251 ATAAAGCATT TTTTTCACCTG CATCTAGTGT GTGGTTTGTC CAAACTCATC
      TATTTTCGTAA AAAAAGTGAC GTAAGATCAA CACCAAACAG GTTTGAGTAG
11301 AATGTATCTT ATCATGTCTG GATCCCACGT GCAGGCGGGG AGGCGGCCCCA
      TTACATAGAA TAGTACAGAC CTAGGGTGCA CGTCCGCCCC TCCGCGGGGT
11351 AAGGGAGATC CCACTCGTCT GAGGGCGAAG GCGAAGACGC GGAAGAGGCC
      TTCCCTCTAG GCTGAGCAGA CTCCCGCTTC CGCTTCTGCG CCTTCTCCGG
11401 GCAGAGCCGG CAGCAGGCCG CGGGAAGGAA GGTCCGCTGG ATTGAGGGCC
      CGTCTCGGCC GTCGTCCGGC GCCCTTCCTT CCAGGCGACC TAACTCCCGG
11451 GAAGGGACGT AGCAGAAGGA CGTCCCGCGC AGAATCCAGG TGGCAACACA
      CTTCCCTGCA TCGTCTTCCT GCAGGGCGCG TCTTAGGTCC ACCGTTGTGT
11501 GGCGAGCAGC CAAGGAAAAG ACGATGATTT CCCCACAAC ACCACGGAAT
      CCGCTCGTCG GTTCCTTTCC TGCTACTAAA GGGGCTGTTG TGGTGCCTTA
11551 TGTCAGTGCC CAACAGCCGA GCCCCTGTCC AGCAGCGGGC AAGGCAGGCG
      ACAGTCACGG GTTGTGCGCT CGGGGACAGG TCGTCGCCCC TTCCGTCCGC
11601 GCGATGAGTT CCGCCGTGGC AATAGGGAGG GGGAAAGCGA AAGTCCCGGA
      CGCTACTCAA GGCGGCACCG TTATCCCTCC CCCTTTCGCT TTCAGGGCCT
11651 AAGGAGCTGA CAGGTGGTGG CAATGCCCCA ACCAGTGGGG GTTGCGTCAG
      TTCTTCGACT GTCCACCACC GTTACGGGGT TGGTCACCCC CAACGCAGTC
11701 CAAACACAGT GCACACCACG CCACGTTGCC TGACAACGGG CCACAACCTC
      GTTTGTGTCA CGTGTGGTGC GGTGCAACGG ACTGTTGCCC GGTGTTGAGG
11751 TCATAAAGAG ACAGCAACCA GGATTTATAC AAGGAGGAGA AAATGAAAGC
      AGTATTTCTC TGTCGTTGGT CCTAAATATG TTCTCCTCT TTTACTTTTCG
11801 CATACGGGAA GCAATAGCAT GATACAAAGG CATTAAAGCA GCGTATCCAC
      GTATGCCCTT CGTTATCGTA CTATGTTTCC GTAATTTTCGT CGCATAGGTG
11851 ATAGCGTAAA AGGAGCAACA TAGTTAAGAA TACCAGTCAA TCTTTCACAA
      TATCGCATTT TCCTCGTTGT ATCAATTCTT ATGGTCAGTT AGAAAGTGTT
11901 ATTTTGTAAT CCAGAGGTTG ATTC
      TAAACATTA GGTCTCCAAC TAAG

```

FIGURE 11-11

Figure 12: Western Blot of Hepsin expressed in 293EBNA cells. 4 days after transfection, conditioned medium was harvested. 10 μ l of conditioned medium was loaded on a 10% Tris-Glycine gel. Untreated 293EBNA cells served as negative control, 5 ng of purified hepsin ED/EK (expressed from insect cells) served as positive control. After electrophoresis, proteins were transferred onto Nitrocellulose membrane at 100 V for 1h. The membrane was then probed with anti-V5 antibody at 37C° for 1h after blocking with 5% dry milk in TTBS buffer for 1h.



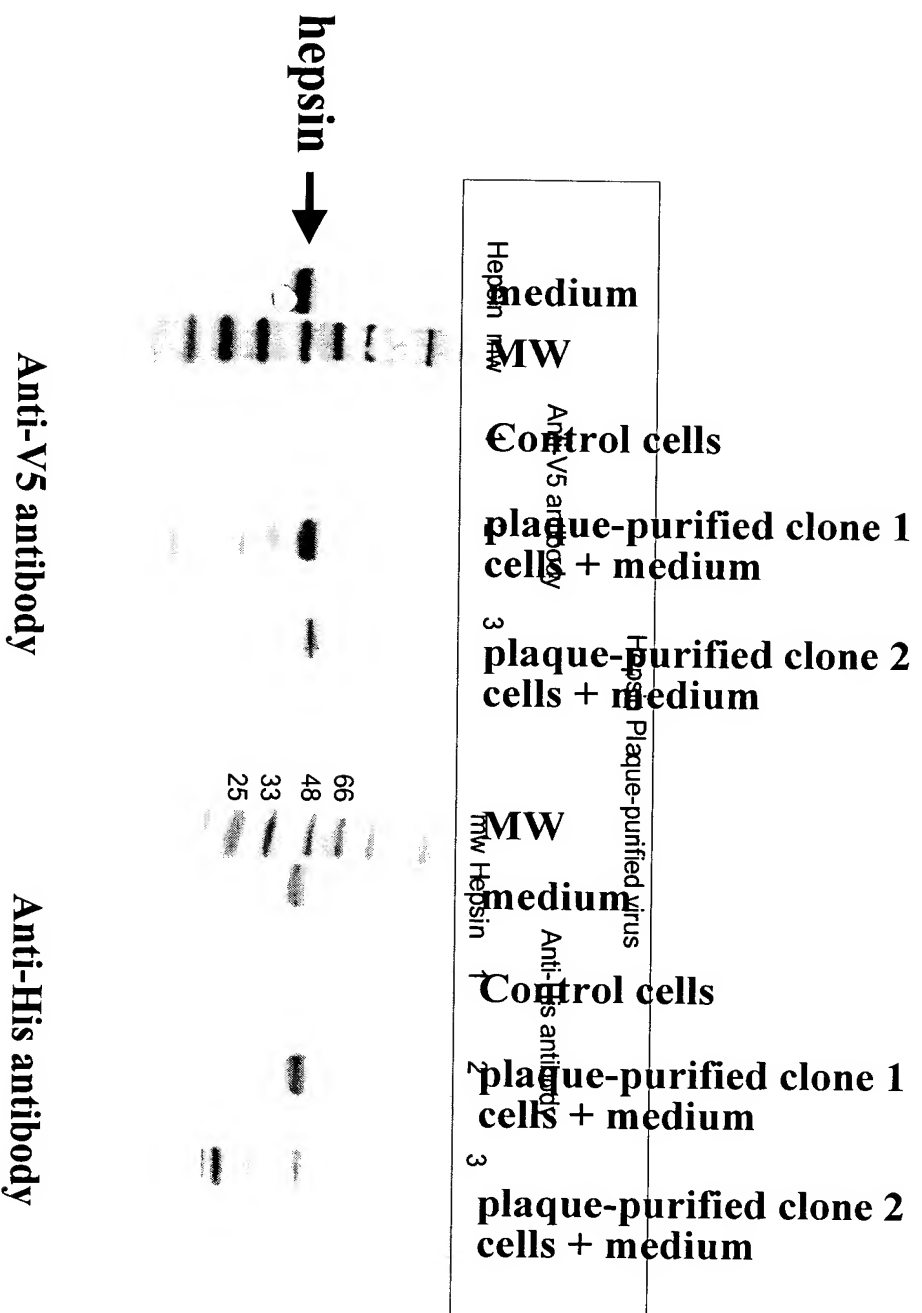
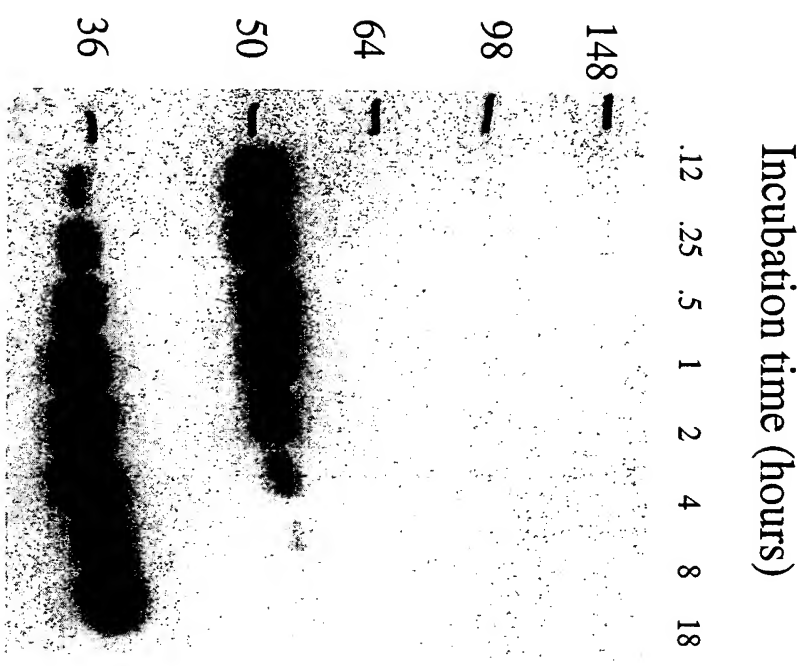


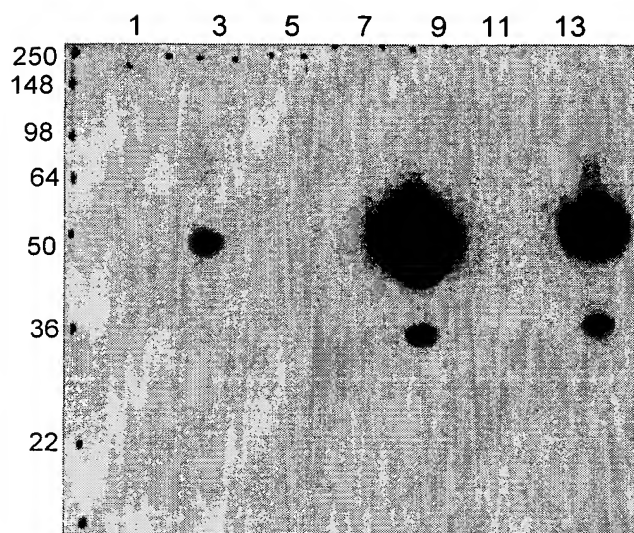
Fig. 13. Western analysis of recombinant soluble hepsin. Recombinant soluble hepsin was expressed in baculovirus infected insect cells. Western analysis using an anti-V5 antibody (left panel) and an anti-His antibody (right panel) showed that recombinant soluble hepsin was present in cultured medium and cell pellets.

Figure 14: Enterokinase (EKMax) processing of Hepsin -ED-EK protein to generate active enzyme



3.1 units EKMax / ml

Figure 15A: Western Slot Blot on the hybridomas 11C1 & 47A5 are WB positive against Hepsin-ED-EK protein.



Blot 1		
slot #	I.D.	CODE
1	1	2F10
2	2	9H6
3	3	11C1
4	4	16A2
5	5	27A1
6	6	30C10
7	7	30H12
8	8	35D4
9	9	47A5
10	10	80F6
11	Blank	
12	Blank	
13	Blank	
14	Mouse Poly clonal	

Figure 15B: Western Slot Blot on the hybridomas 31C1 and 38E2 are WB positive against Hepsin-ED-EK protein.

Blot 1		
slot #	I.D.	CODE
1	1	7H3
2	2	12A2
3	3	16A3
4	4	20D1
5	5	22A3
6	6	31C1
7	7	31H2
8	8	36B2
9	9	38 E2
10	10	39D6
11	11	41F7
12	12	42 E3
13	Blank	
14	Mouse Poly clonal	

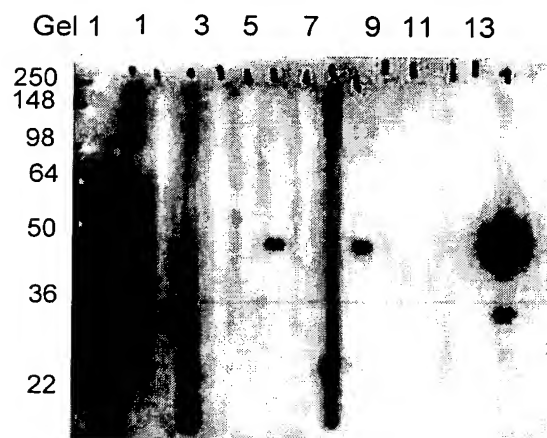
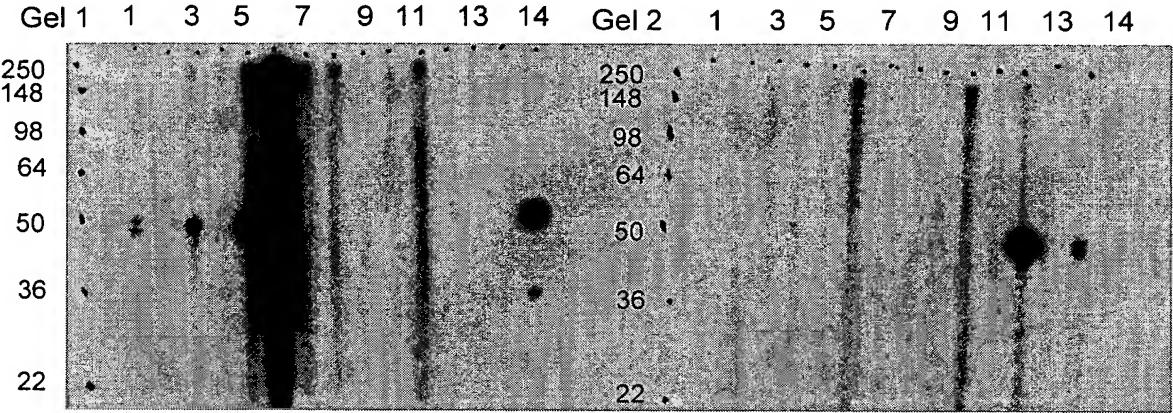


Figure 15C: Western Slot Blot on the hybridomas 37G10, 46D12 & 14C7 are WB positive against Hepsin-ED-EK protein.



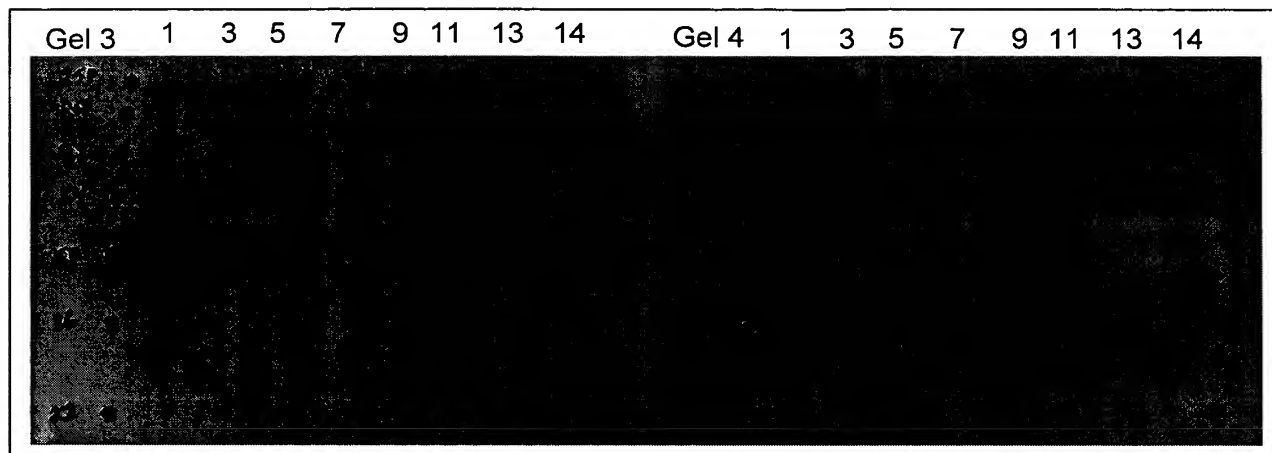
Gel 1

Slot	Sample	Dilution
1	Rabbit Polyclonal –Cayman Chem	1:500
2	Media	neat
3	37G10	"
4	94A7	"
5	46D12	"
6	103E3	"
7	40F1	"
8	103H12	"
9	93D1	"
10	10C2	"
11	102F2	"
12	83E11	"
13	Blank	
14	Blank	
15	Protein - ♂ mouse	1:5000

Gel 2

Slot	Sample	Dilution
1	Protein - ♂ mouse	1:5000
2	Media	neat
3	27E7	"
4	92A7	"
5	91A4	"
6	99B11	"
7	94C7	"
8	91A1	"
9	14H11	"
10	74C7	"
11	72H6	"
12	14C7	"
13	Blank	
14	Rabbit Polyclonal –Cayman Chem	1:500

Figure 15D: Western Slot Blot on the hybridomas 14C7 & 72H6 are WB positive against Hepsin-ED-EK protein.



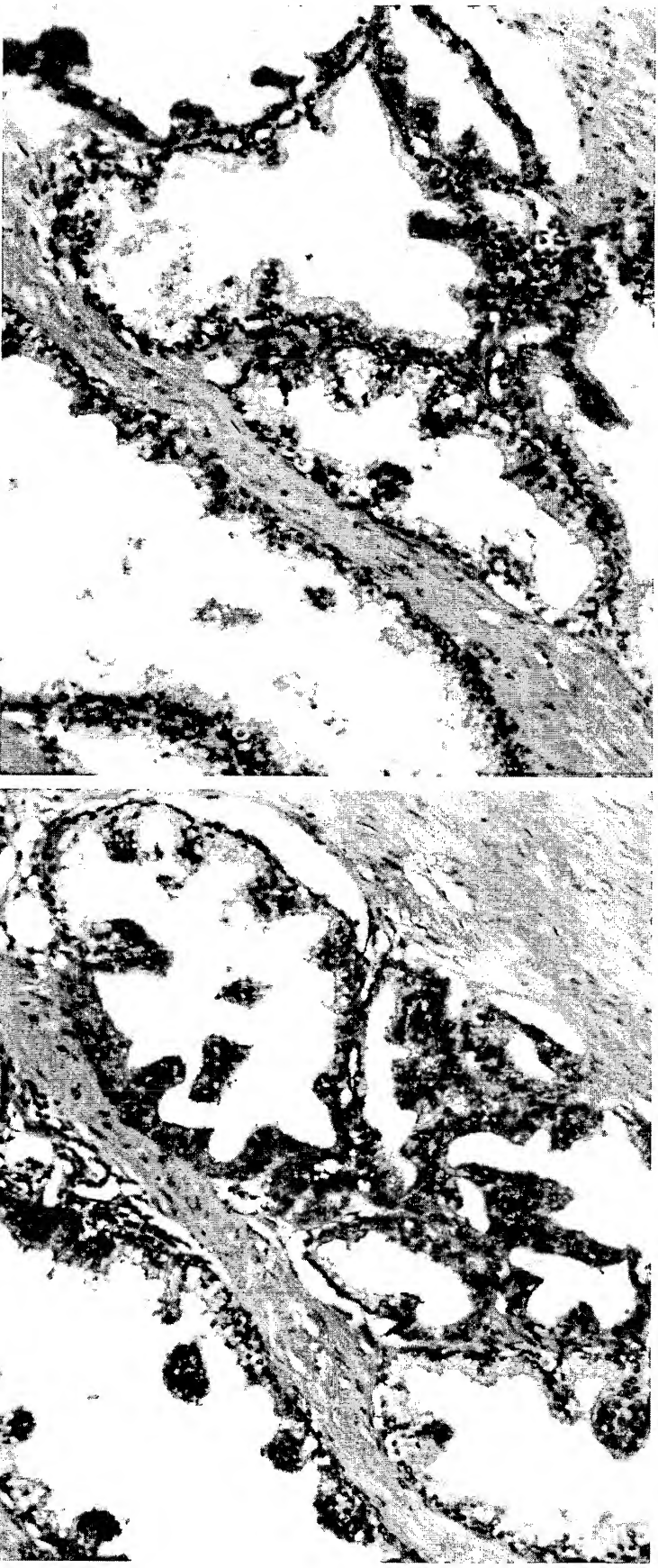
Gel 3

Slot	Sample	Dilution
1	Protein - ♂ mouse	1:5000
2	Media	neat
3	84G6	"
4	84H2	"
5	51F8	"
6	15b11	"
7	90E6	"
8	72H6	"
9	85A4	"
10	87C2	"
11	3G11	"
12	53E11	"
13	91H4	"
14	53C7	"
15	88C7	"

Gel 4

Slot	Sample	Dilution
1	Protein - ♂ mouse	1:5000
2	Media	neat
3	75H3	"
4	98B4	"
5	91C9	"
6	53D9	"
7	80G6	"
8	95F3	"
9	14C7	"
10	80H10	"
11	92A9	"
12	81C8	"
13	96B6	"
14	18I2	"

FIG 16A: Human Prostate Tumor Tissue



Control
Anti-Hepsin mouse
polyclonal preimmun
1/500 (9)

Anti-Hepsin mouse
polyclonal immun
1/500 (10)

FIG 16B: Human Prostate Tumor Tissue

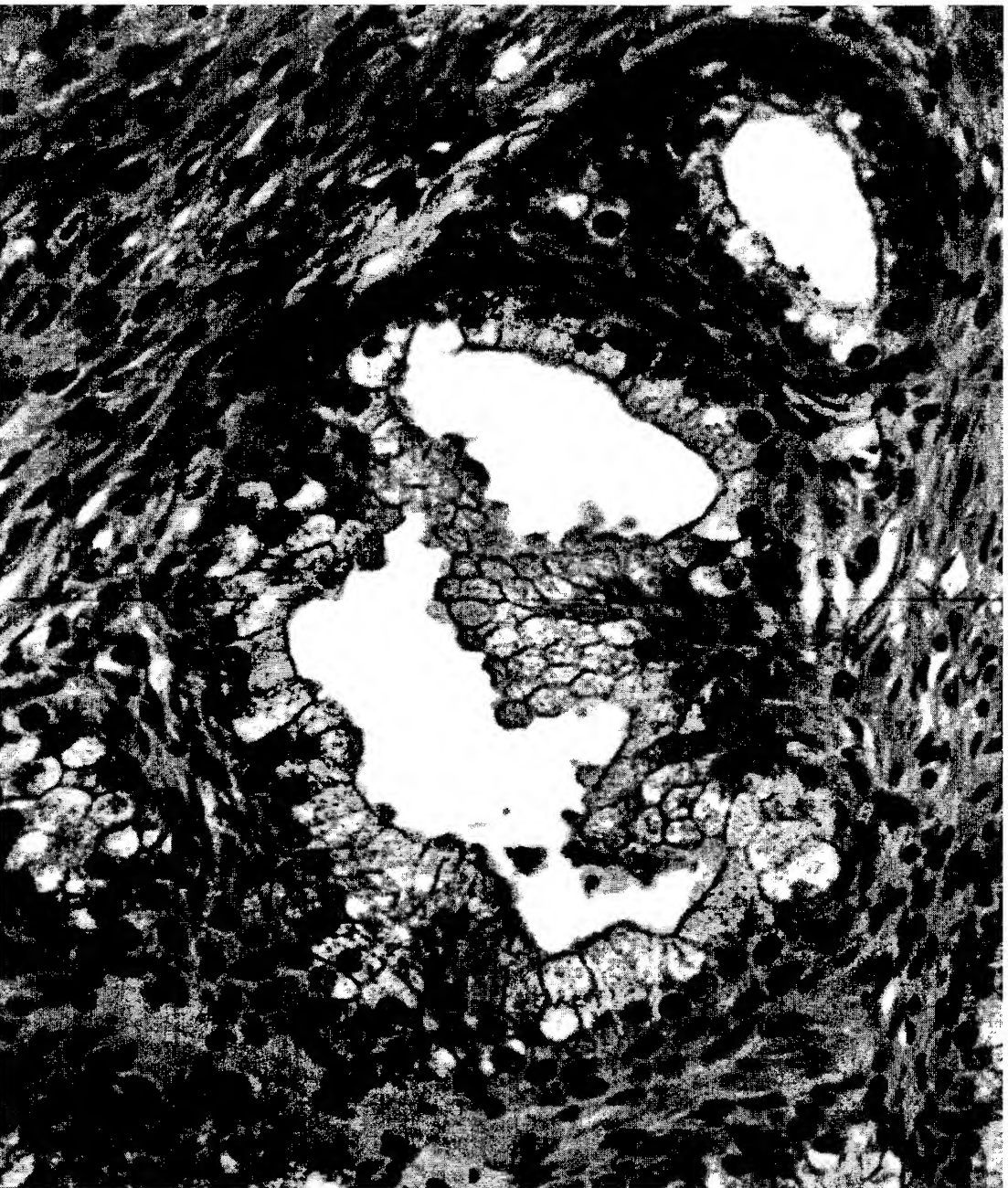


Control medium



Anti-Hepsin monoclonal ab (medium)

FIG 16C: Human Prostate Tumor Tissue



Anti-Hepsin monoclonal ab

Figure 17

Human wild-type hepsin amino acid sequence:

```
maqkeggrtv pccsrpkvaa ltagtllllt aigaaswaiv avllrsdqep lypvqvssad 61
arlmvfdkte gtwrllcssr snarvagls eemgflralt hseldvrtag angtsgffcv 121
degrlphtqr llevisvcdc prgrflaaic qdcgrrklpv drivggrdts lgrwpwqvs1 181
rydgahlcgg sllsgdwvlt aahcfpernr vlsrwrvfag avaqasphgl qlgvqavvyh 241
ggylpfrdpn seensndial vhlssplplt eyiqpvclpa aggalvdgki ctvtgwgn1tq 301
yygqqagvlq earvpiisnd vcngadfygn qikpkmfcag ypeggidacq gds1ggpfvce 361
dsisrtprwr lcgivswgtg calaqkpgvy tkvsdfrewi fqaikthsea sgmvtql
```

the cytoplasmic domain: Met1 to Lys17

the transmembrane domain: Val18 to Leu44

the ectodomain: Arg45 to Leu417

Figure 18

Hep-ED-EK structure (modified soluble hepsin with substitute activation sequence)

```
1  RSDQEPLYPV QVSSADARLM VFDKTEGTWR LLCSSRSNAR VAGLSCEEMG FLRALTHSEL
61 DVRTAGANGT SGFFCVDEGR LPHTQRLLEV ISVCDPCRGR FLAAICQDCG RRKLPVDDDD
121 KIVGGRDTSL GRWPWQVSLR YDGAHLCGGS LLSGDWVLTA AHCFPERNRV LSRWRVFAGA
181 VAQASPHGLQ LGVQAVVYHG GYLPFRDPNS EENSNDIALV HLSSPLPLTE YIQPVCLPAA
241 GQALVDGKIC TVTGWGNTQY YGQQAGVLQE ARVPIISNDV CNGADFYGNQ IKPKMFCAGY
301 PEGGIDACQG DSGGPFVCED SISRTPRWRL CGIVSWGTCG ALAQKPGVYT KVSDFREWIF
361 QAIKTHSEAS GMVTQLEFGK PIPNPLLGLD STRTGHHHHH H*
```

Cytoplasmic domain: absent

Transmembrane domain: absent

Modified activation domain:117-121 (underlined)

V5 and 6-His Tag: 377-401

Figure 19

Antibody Neutralization

